

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 10:04:22 ; Search time 52 Seconds
(without alignments)
4908.735 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSTTKNVKVPICENNEN.....PSAEGGEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	4234	100.0	809 4 Q9NQW8	Q9NQW8 homo sapien
2	3181.5	75.1	782 6 Q8MJD7	Q8mjd7 canis fami
3	3166.5	74.8	610 4 Q9NRE9	Q9NRE9 homo sapien
4	2515	59.4	694 11 Q9JUJ29	Q9juz29 mus musculu
5	1971.5	46.6	866 11 Q80XL8	Q80xl8 mus musculu
6	1959	46.3	1339 11 Q35788	Q35788 rattus norv
7	1952	46.1	1245 4 Q43636	Q43636 homo sapien
8	1949	46.0	1251 4 Q9UMG2	Q9umg2 homo sapien
9	1923	45.4	858 11 Q55157	Q55157 rattus norv
10	1920	45.3	938 6 Q77659	Q77659 bos taurus
11	1920	45.3	948 6 Q77659	Q77659 bos taurus
12	1920	45.3	952 6 Q77659	Q77659 bos taurus
13	1103	26.1	1037 5 Q9W2D5	Q9w2d5 drosophila
14	1103	26.1	1040 5 Q8IH43	Q8ih43 drosophila
15	1096	25.9	800 5 P90975	P90975 caenorhabdi
16	1095	25.9	800 5 Q62237	Q62237 caenorhabdi

ALIGNMENTS

RESULT 1

Q9NQW8 PRELIMINARY; PRT; 809 AA.
AC Q9NQW8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cone photoreceptor cyclic nucleotide-gated channel beta subunit.
GN CNGB3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20414632; PubMed=10958649;
RA Kohl S., Baumann B., Broghammer M., Jagle H., Sieving P., Kellner U.,
RA Spegal R., Anastasi M., Zrenner E., Sharpe L.T., Missinger B.,
RT "Mutations in the CNGB3 gene encoding the Beta-subunit of the cone
RT photoreceptor cGMP-gated channel are responsible for achromatopsia
RT (ACHM3) linked to chromosome 8Q21.";
RL Hum. Mol. Genet. 9:2107-2116(2000).
DR EMBL; AF272900; AAF66274.1; --
DR Genew; HGNC:2153; CNGB3.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; P:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; CNMP_binding; 1.
DR Pfam; PF00320; ion_trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.

17 878 20.7 515 5 Q95SL0
18 818 19.3 686 6 Q9N0H4
19 806 19.0 611 11 Q9QWV7
20 806 19.0 632 11 Q9ER32
21 806 19.0 670 11 Q9ER33
22 789.5 18.6 664 11 Q80XH6
23 788.5 18.6 631 11 Q8CFV6
24 787.5 18.6 1218 5 Q9W201
25 783.5 18.5 637 13 Q804I6
26 759 17.9 1463 5 Q9USE2
27 746 17.6 900 5 Q971I9
28 723 17.1 1324 5 Q8IR35
29 714.5 16.9 737 13 Q8UVT8
30 712 16.8 609 13 Q8JFP0
31 703 16.6 551 13 Q8JFN9
32 702.5 16.6 310 11 Q80VQ4
33 702 16.6 1696 5 Q9VXV8
34 621 14.7 147 11 Q9QWK1
35 563.5 13.3 695 5 Q93486
36 536 12.7 474 4 Q8IV77
37 509 12.0 832 5 Q9N4C1
38 478 11.3 252 11 Q9QX26
39 441.5 10.4 644 5 Q51827
40 400 9.4 774 4 Q86WJ5
41 383 9.0 945 5 Q971J9
42 383 9.0 1327 5 Q9V702
43 381 9.0 678 5 Q96777
44 375 8.9 767 5 Q76977
45 369.5 8.7 890 4 Q86WJ6

Q95SL0 drosophila
Q9N0H4 sus scrofa
Q9QWV7 rattus norv
Q9ER32 rattus norv
Q9ER33 rattus norv
Q80XH6 mus musculu
Q8CFV6 mus musculu
Q9W201 drosophila
Q804I6 carassius a
Q9USE2 drosophila
Q971I9 limulus pol
Q8IR35 drosophila
Q8UVT8 oncorhynch
Q8JFP0 ictalurus p
Q8JFN9 ictalurus p
Q80VQ4 mus musculu
Q9VXV8 drosophila
Q9QWK1 rattus norv
Q93486 caenorhabdi
Q8IV77 homo sapien
Q9N4C1 caenorhabdi
Q9QX26 rattus norv
Q51827 caenorhabdi
Q86WJ5 homo sapien
Q971J9 drosophila
Q9V702 drosophila
Q96777 heliothis v
Q76977 strongyloe
Q86WJ6 homo sapien

599	Qy	GGGRTNTANVAHGPFANLLTDDKKTLOBILVHYDPDSRILMKKARVLLKQKATAETPP	658
594	Db	RGGNRTANVAHGPFANLLTDDKKTLOBILVHYDPSEKILMKKASVLLKKKAPATETPP	653
659	Qy	RDXDLLPPPKETPKLFTKLGGTGKASIALRLKLREQAOKKENSEGCEBEGKENEED	718
654	Db	RKGLAFLPPPKQETPKIFALLGGTGKAGLTRLILKLREQTIQK--TSENSEGG	706
719	Qy	KOKENEDKOKENEDKGENEDKDKGREPEEKPLDRPCTASPIAVEBEPHSVRTVLPGR	778
707	Db	-----GKREYEDKERESEKILDSSECRANCIIAEMPQISRAALPRG	751
779	Qy	TSROSLIISMAPSAGGSEVLTIEVKEKAKQ	809
752	Db	TTROSLIISMAPSAGGSEVLTIEVKEKAKQ	782

RESULT 3

Q9NRE9 PRELIMINARY; PRT; 610 AA.

Q9NRE9;
AC 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cone photoreceptor cGMP-gated cation channel beta-subunit.
GN CNGB3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=20347712; PubMed=10888875;
RA Sundin O.H., Yang J.-M., Li Y., Zhu D., Hurd J.N., Mitchell T.H.,
RA Silva E.D., Maumenee I.H.;
RT "Genetic basis of total colourblindness among the Pingelapese
islanders";
RT Nat. Genet. 25:289-293(2000).
RL ENEL; AF228520; RAFA0179.1; -
DR GO; GO:0007601; Pivision; TAS.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K+channel_pore.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; 1.
DR PROSITE; PS00042; cNMP_BINDING_3; 1.
DR K0 Ionic channel; Receptor; Transmembrane.
SW SEQUENCE 610 AA; 70039 MW; 843B01F12643B73A CRC64;

	Query Match	74.8%;	Score 3166.5;	DB 4;	Length 610;
	Best Local Similarity	99.0%;	Prod. No. 5.7e-214;		
	Matches 609;	Conservative 0;	Mismatches 1;	Indels 5;	Gaps 1;
Qy	195	MPLTEYIKRIKLPNSIDSYDRLYLLMLLLIYLAANNWCNFIPLRLVPYQTADNIHWL	254		
Db	1	MPLTEYIKRIKLPNSIDSYDRLYLLMLLLIYLAANNWCNFIPLRLVPYQTADNIHWL	60		
Qy	255	IADIICDIYLYDMLFIQPLRQFVRGSDIIVDSNELRKHYRTSTKFLQDVASIIIPFDICY	314		
Db	61	IADIICDIYLYDMLFIQPLRQFVRGSDIIVDSNELRKHYRTSTKFLQDVASIIIPFDICY	120		
Qy	315	LFEGFNPMFRANRLKYSFEEFNHLEISMDKAYIVRIITGTGYLLFIILINACVYWA	374		
Db	121	LFEGFNPMFRANRLKYSFEEFNHLEISMDKAYIVRIITGTGYLLFIILINACVYWA	180		
Qy	375	SNYEGIGTRVYVYDGEAGNEYLRCYYWVRTIITIGLPEPOTLPEIVPOLNLFSGVEVF	434		
Db	181	SNYEGIGTRVYVYDGEAGNEYLRCYYWVRTIITIGLPEPOTLPEIVPOLNLFSGVEVF	240		

QY	435	SSLIQOMEDVIGAAATANONYFRACWDDTTIAYMNNYSIPKLQKRVRTWYETWDSORMLD	499
Db	241	SSLIQOMEDVIGAAATANONYFRACWDDTTIAYMNNYSIPKLQKRVRTWYETWDSORMLD	300
QY	495	ESDLTKTLFTTVALALADNVNFSIISKVDLPKCDTQMIYDMLRLKLSVLYLPDGFVCKK	554
Db	301	ESDLTKTLFTTVALALADNVNFSIISKVDLPKCDTQMIYDMLRLKLSVLYLPDGFVCKK	360
QY	555	GGIGKEMVIIKHGEVONLGGPDGKVLAVTLKAGSVTGEISLLAAGGNNRTANVAHGFA	614
Db	361	GGIGKEMVIIKHGEVONLGGPDGKVLAVTLKAGSVTGEISLLAAGGNNRTANVAHGFA	415
QY	615	NLLTLDKTKTLQEBILVHYPDSEIRILMKKARVLLKQAKTAEPATPPKDLALLFPPEETPK	674
Db	416	NLLTLDKTKTLQEBILVHYPDSEIRILMKKARVLLKQAKTAEPATPPKDLALLFPPEETPK	475
QY	675	LPKTLGGTGKASTARLLKLKEQAOKKNSGEGEEGKKNEDKOKENEDKOKENEDK	734
Db	476	LPKTLGGTGKASTARLLKLKEQAOKKNSGEGEEGKKNEDKOKENEDKOKENEDK	535
QY	735	KENEDKDKGREPEEKPLDRPECTASPIAVSEEPHSVARTVLPRTGTSRQSLIISMAPSASG	794
Db	536	KENEDKDKGREPEEKPLDRPECTASPIAVSEEPHSVARTVLPRTGTSRQSLIISMAPSASG	595
QY	795	GSEVLITIEVKEKAKQ	809
Db	596	GSEVLITIEVKEKAKQ	610

RESULT 4

Q9JUZ9 PRELIMINARY; PRT; 694 AA.

ID Q9JUZ9

AC Q9JUZ9

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Cyclic nucleotide-gated channel subunit CNGc.

OS CNGB3 OR CNGc.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

FC MEDLINE=C57Black6;

FX STRAIN=C57Black6;

RA Garstner A., Zong X., Hofmann F., Biel M.;

RT Molecular Cloning and Functional Characterization of a New Modulatory

RL Cyclic Nucleotide-Gated Channel Subunit from Mouse Retina.,"

RL J. Neurosci. 20:1324-1332 (2000).

DR EMBL; AJ243572; CAB71152.1;

DR MGD; MGI:1353562; Cngb3.

DR GO; GO:0005886; C:plasma membrane; IC.

DR GO; GO:0030553; F:3', 5'-cGMP binding; IC.

DR GO; GO:0005223; F:intracellular cGMP activated cation channel. . .; IPI.

DR GO; GO:0009187; P:cyclic nucleotide metabolism; IC.

DR InterPro; IPR000595; cNMP binding.

DR InterPro; IPR005821; Ion trans.

DR Pfam; PF00027; cNMP binding; 1.

DR Pfam; PF00520; ion trans; 1.

DR SMART; SM00100; cNMP; 1

DR PROSITE; PS00888; cNMP_BINDING_1; 1.

DR PROSITE; PS00889; cNMP_BINDING_2; 1.

DR PROSITE; PS00042; cNMP_BINDING_3; 1.

DR Ionic channel; Transmembrane.

SW SEQUENCE 694 AA; 0B9F9CF3B180DA82 CRC64;

Query Match

Query Match
Best Local Similarity
59.4%; score 2315; DB II,
68.7%; Pred. No. 4.1e-168;

BEST LOCAL SIMILARITY	88.7%	FREQ. NO.	4.1E-100
MATCHES	485	CONSERVATIVE	92
		MISMATCHES	113
		INDELS	16
		GAPS	7

OV 1 MFKSLT-KVKVKPIGENNENEQSSRRNEEGSHP--SNQSQQTAAQENKGEEKSLKTKS 57

Db 1 MLKSLTVKFNKVPNPM-----EGRMKKLCPNLSSLSQPTIAQDGNQSEKEPLRSR- 50
QY 58 TPVTSEEPHTNIQDKLSKNSGDLTTPDPQNAABPTGTVPEQKMDPGKEGNSPQNK 117
Db 51 TPITFEKSHSK-EDNSTGNSLDFTPNPDPECAELTRTMAEKRTRTKGERVSPFKT 109
QY 118 PPAAPVINEYADAQHLNVLKMRORTALYKXKLVEGD--LSPEASPTAKTAVPPVKES 176
Db 110 VLETSIINEYTDALHNLVEMRERETALYKXKLTBEENFPVEASSQTAMSTNISPQEN 169
QY 177 DDKPTHEYRLLWFKVKOMPTEYLKRIKLNDSIDSTDRLLYLLWLLVLTAYNNWCWF 236
Db 170 NSKLKEH-QDTFSEKPPQVPEKHLRMLRSDISYTDVYLLWLLVLTAYNNWCWL 228
QY 237 PLRLVFPYQTDADNTHYMLADIICDIIYVLMFIQRLQVPGDGIIVDSNELRKHRT 296
Db 229 PVRLVFPQTDNKNYWIITDIVDIIYVLDIILQRLQVPGGEIIVDSNELRKHRTS 288
QY 297 STKQLDVASIIPEDICYLFGFNPFRANRLKXTSFFPNHLESIMDKAYIRVIRT 356
Db 289 STKFRMDVASLLPEVLYIFFGVNPPIFRANRLKXTSFFPNHLESIMDKAYIRVIRT 348
QY 357 TGYLLFLHINACVYVNASVEGIGTTRWYDGEVNEVLYRYWAVTLITIGLPEPOT 416
Db 349 TGYLLFLHINACVYVNASVEGIGTTRWYDGEVNEVLYRYWAVTLITIGLPEPOT 408
QY 417 LFEIVFQNLNFGSVFSSLIQMDVIGAAATANQNYFRACMDTIAYNNYSIPKLQV 476
Db 409 SFEIVFQNLNFGSVFSSLIQMDVIGAAATANQNYFRACMDHIAYNNYSIPQSVQ 468
QY 477 KRVTWYTWDSQMSDESLKLTTLTTLVLAIDVNSIISKVDLFGKCDTQMIDYM 536
Db 469 YRVTWLWYVNSQRIIDENLLENPTAQSLTALDINFSIIDKVELFPGKCDTQMIDYL 528
QY 537 LLRLKSLVLPDGFCKGKEIGKEMWIIKHGEVOVLGGPDGTVLTLKAGSVFGEISLL 596
Db 529 LLRLKSLVLPDGFCKGKEIGKEMWIIKHGEVOVLGGPDGTVLTLKAGSVFGEISLL 588
QY 597 AAGGNRTANVAHGPFANILTLDKTLQELVHYPSERILMKARVLVKKAKATAEAT 656
Db 589 AKGNGERTADVAGHPFANILTLDKTLQELVHYPSERILMKARVLVKKAKATAEAT 648
QY 657 PPRKDLALLPPKKEETPKLTKTLGGTGKASLAFLLKXEQAAQK 702
Db 649 PARPGPALFPKKEETPRMLKVLGNTGKVDLGLLKGKRTTQK 694

RESULT 5

Q80XL8 PRELIMINARY; PRT; 866 AA.
AC Q80XL8
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE LOC333329 protein (Fragment).
GN LOC333329.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
FN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Eve;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eve;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045114; AHA45114.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; P:ion channel activity; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00027; CNMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS00442; CNMP_BINDING_3; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
FT NON_TER 1
SQ SEQUENCE 866 AA; 97427 MW; CACC4AD8EBDEE2A CRC64;

Query Match 46.6%; Score 1971.5; DB 11; Length 866;
Best Local Similarity 47.5%; Pred. No. 8.5e-130;
Matches 406; Conservative 107; Mismatches 247; Indels 95; Gaps 14;
QY 21 EQSSRRNEEGSHPSNQSOQTAAQENKGEESLTKTSPVTSEEPHTNIQDKLSKNSG 80
Db 38 EBKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEE 94
QY 81 DL-----TTNPDQNAABPTGTVPEQKMDPGKEGPN-----SPQNKPPAA 121
Db 95 PLIPEETLPPPPPPSPVKSDTLTPGAAAAGHRKKLPQQDDEAEELKALSPAESPVVA 154
QY 122 ---PVINEYADAQ-----LHNLVXMRQRTALYKXKLVEGDLSSPEAS 161
Db 155 WSDPTTQEAADQDRAASTASQNSALINDRLQELVKMFKEKTEKVKELIDPDVTSDEES 214
QY 162 POTAKPTAVPVKESDDKPT-----EHYRLLWFKVMKMPLEYLKRILKLPNSIDSYT 214
Db 215 PKPS-PAKKAPEPDPAKPAEAEVAEEHYCDMLCKFKRRLPNY---RFQSIDPLT 269
QY 215 DRVLLWLLVLTAYNNWCNPIPLRVFPYOTADNIHYWLIADICDIIYVLMFIQPR 274
Db 270 NLMWILWLFVVLANNWCNLIPIVWAFPIYORADNIHFWLLMDYLCDFIYLLDITVQMR 329
QY 275 LQFVRGGDIIIVDSNELRKHRTSTKFDQVNASIIPFDICYLFGFNPFRANRLKXTSF 334
Db 330 LQFVKGDDIITDKEMRNLYKSRFRKMDLCLLPDLFLVYKLGINLPLRCLKYNMF 389
QY 335 FEENHLESINDKAVIRVIRTTCTYLLFILHINACVYVNASVEGIGTTRWYDGEVNE 394
Db 330 FEENRLEALISKAYIRVIRVINTTAYLLSYLHNSCLYMASAFQIGSTHWIDVGNYS 449
QY 395 LRCYTWAVRLLITIGLPEPOTLEFEIVFQNLNFGSVFSSLIQMDVIGAAATANQNY 454
Db 450 IRCYTWAVRLLITIGLPEPOTLEFEIVFQNLNFGSVFSSLIQMDVIGAAATANQNY 509
QY 455 FRACMDTIAYNNYSIPKLKVLGNTGKVDLGLLKGKRTTQK 514


```
Db 510 YRSCDSTVKYNNFYKIPRSVQNRVKTWYETWHSQGMDESELMVQPDKRLDLAIDV 569
QY 515 NFGIISKVDLFGKCDTQMIYDMLRLKLSVLYLPDGFVCKKGIGKEMYIIKHGEVQVLGG 574
Db 570 NYSIVSKVALFGQCDQMIYDMLRLKLSVLYLPDGFVCKKGIGKEMYIIKHGEVQVLGG 629
QY 575 PDGKVLVTLKAGSVFGEISLLAAGGNNRTANVAHGFANLLTLDKTLQBLVHYHYPDS 634
Db 630 PDGKVLVTLKAGSVFGEISLLAAGGNNRTANVAHGFANLLTLDKTLQBLVHYHYPDS 689
QY 635 ERTLMKARVLLKOKAKTAEATPPRDLALLPDPKEETPKLFTLGGTGKAS----- 687
Db 690 QKLRKARMLNNK-----PKESKSVLILPPRAGTPKLFWAALAAAGKMPGKAGG 744
QY 688 -----LARIKLKREQAA-----OKXNSGEGEEBKEDKOKENEDK 734
Db 745 KLAHLARLKLAAALAAARQQQLLEQAKSQSAGGEGSGATDQAPQEP----- 795
QY 735 KENEDKDKGREPEKELDRPECTASPIAVEEBPHSVRRTVLPRGTSRQSLIISMAPSABG 794
Db 796 PEPKDPKPPGPE-----PSAOSPPASAKPE--ESTGEAAGPPEPSVRIEVSPPDP 848
QY 795 GEEVLATIEVKEKAKQ 809
Db 849 GEOTLSVEVLEEKKE 863

RESULT 6
ID 035788 PRELIMINARY; PRT; 1339 AA.
AC 035788;
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DE 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Cyclic nucleotide-gated channel beta subunit.
CN CNG4.1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Sautter A., Biel M., Hofmann F.;
RT "Molecular cloning of cyclic nucleotide-gated cation channel subunits
RT from pineal gland";
RL Mol. Brain Res. 47:171-175 (1997).
DR EMBL; AJ000496; CAA04133.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR000595; C:GMP binding.
DR InterPro; IPR005821; I:ion trans.
DR Pfam; PF00027; C:GMP binding; 1.
DR Pfam; PF00520; I:ion trans; 1.
DR SMART; SM00100; C:GMP; 1.
DR PROSITE; PS00888; C:GMP_BINDING_1; 1.
DR PROSITE; PS00889; C:GMP_BINDING_2; 1.
DR PROSITE; PS50042; C:GMP_BINDING_3; 1.
KW Ionic channel; Transmembrane
SQ SEQUENCE 1339 AA; 151046 MW; FFAD64A6A81AB49A CRC64;

Query Match 46.3%; Score 1959; DB 11; Length 1339;
Best Local Similarity 46.3%; Pred. No. 1.2e-128;
Matches 400; Conservative 121; Mismatches 240; Indels 102; Gaps 15;

QY 11 VKPTGNNENQSRNREGSHPSNQSQITQAQENKGEESLTKSTPTVTSPEPHNIQ 70
Db 512 IQELPEEEKEEKEEKEE-----EKEEKEEKEEKEEKEEATNSTVPAIKHEPELOVE 568
QY 71 DKLSKQSSGDLTNPDPQN-----AAEPTGTVP-----EQKMDPQG 108
```

```
Db 569 DTDAAAGPLIPEETIPPERPPVSPAKSDTLAVPSAATHRKKLPSQDDEAEELKALSPAE 628
QY 109 -----EGPNSPQ-----NKPPAAPVINEYADAQLHNLVKRMQRTALYKKKLIVE 152
Db 629 SPVVAWSDPITPQADGEDRAASTASQNSAIID-----RLQELVKMFKERTKVKERKLD 684
QY 153 GDLS-----SPASQOTAKPTAVPVK--ESDDKTEHYVRLWPKVKKMPLELYKRIKL 206
Db 695 PDVTSDESPKSPAKAPDSAPAKPAEAAEAEHCDMLCKCFKRRPWKM-----QF 740
QY 207 PMSDSVYDRLYLWLLVTLAYNNWCMFIPRLRFPFYQYADNHYHLLADIICDIIVLY 266
Db 741 PQSIDPLTNLMYILWLFVFLAMNWCWLPVRWAFYQYADNHYHLLADIICDIIVLY 800
QY 267 DMLFPIQLPQVRGGDIIVDSNELRKHYRTSTKFDLVASIIIPDICVLPFGFENPMFRAN 326
Db 801 DITVQMRQLQVKGDDIITDKKERNNYLSQRFMDLLCLLPDLPFLYKLGVPFLRLP 860
QY 327 RMLKYTSFEFENHLESIMDKAYIYRVIRTTGYLLFILHNACVYVWASNVGEGTTRTW 386
Db 861 RCLKYMAFFENNRLEAILSXAYVVRVIRTTAYLLYSLHNSCLYYWASAFQGGSTHW 920
QY 387 YDGEVNEVLRVYVAVRTLITIGLPEPOTLFEIVFOLLNPFSGVVFESSLIGQVRDVG 446
Db 921 YDGVNSYIRCYWAVKTLITIGLPPDPTLFEIVFOLLNFTGTVAFSVMIQNRDVG 980
QY 447 AATANQYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRMDESDLLXLTPTV 506
Db 981 AATAGQTYRSCDSTVKYNNFYKIPRSVQNRVKTWYETWHSQGMDESELMVQPDK 1040
QY 507 QLAALAVNFSIIISKVDLFGKCDTQMIYDMLRLKLSVLYLPDGFVCKKGIGKEMYIIKH 566
Db 1041 RLIDLADVNYNTSVKVALFGQCDQMIYDMLRLKLSVLYLPDGFVCKKGIGREMYIIQA 1100
QY 567 GEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGGNNRTANVAHGFANLLTLDKTKTQE 626
Db 1101 GQVQVLGGPDGKAVLVTLKAGSVFGEISLLAAGGNNRTANVAHGFANLLTLDKTKLNE 1160
QY 627 ILVHYPSDSERILMKARVLLKOKAKTAEATPPRDLALLPDPKEETPKLFTLGGTGKA 686
Db 1161 ILVHYPSOKLRRKARMLNNK-----PKESKSVLILPPRAGTPKLFWAALAAAGK 1215
QY 687 S-----LARIKLKREQAA-----OKXNSGEGEEBKEDKOKENEDK 726
Db 1216 GPRGAKGKLHLARLKLAAALAAARQQQLLEQAKSQSAGGEGSGATDQAPQPS 1275
QY 727 QKENEDKGENEDKDKGREPEKELDRPECTASPIAVEEBPHSVRRTVLPRGTSRQSLI 786
Db 1276 -----EPKEPP--EPPAPSSPPASAKPEG--STEEAAGPPPSVRI 1313
QY 787 SWAPSABGEEVLTIEVKEKAKQ 809
Db 1314 RVSPGDPGEOTLSVEVLEEKKE 1336

RESULT 7
ID 043636 PRELIMINARY; PRT; 1245 AA.
AC 043636;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Rod photoreceptor CNG-channel beta subunit.
CN RCN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Grunwald M.E., Yu W.P., Yu H.H., Yau K.W.;
RT "Identification of a domain on the beta subunit of the rod cGMP-gated
RT cation channel that mediates inhibition by calcium-calmodulin.";
```


DR PROSITE; PS50042; CNMP_BINDING_3; 1.
SQ Ionic channel; Transmembrane.
KW SEQUENCE 948 AA; 105212 MW; 1DA77400115C2074 CRC64;

Query Match 45.3%; Score 1920; DB 6; Length 948;
Best Local Similarity 45.9%; Pred. No. 4e-126;
Matches 401; Conservative 118; Mismatches 242; Indels 112; Gaps 17;

QY 15 GENNEEQSSRRNEGSHPSNOSQQTAAEENKGEKSILKTSPTVTEEPHTNIQDK-- 72
Db :
QY 86 GAQAQGEVGGAQGDGVGGA-QDQSTSHQELQ--BEALADSGVPATEEHPELQVEDADA 142
Db :
QY 73 -----LSKNSSGDLTNPDPQNAAEPTGTVP-----EQEMDPGK 108
Db :
QY 143 DSRPLIAEENPPSPVOLPLSP--AKSDTLAVPGSATGSIRKLRLPSQDDAEELKMLSPAA 200
Db :
QY 109 -----EGNSPQNKPPA-----APVINEYADAQLHNLVKRMQORTALYKKLVE 152
Db :
QY 201 SPVAWSDDPTSFGTDQDQDRASTRATSONSAIIND---RLQELVKLFERTEKVEKLIID 256
Db :
QY 153 GDLS-----SPEASPTAKTAVPPVK--ESDDKPTEHYRLLFWFKWKMPLTEYLKRKL 206
Db :
QY 257 PDVTSEDESKPKSPAKPAPEPAPEVKAAGOVEEBHEHCMLCKCFKRPWKKY----QF 312
Db :
QY 207 PMSIDSYTRLYLMLLLLVLAYNNWCNFIPIRLVFPYQTADNIHYWLADIICDIIVLY 266
Db :
QY 313 PQSIDPLTNLMYLWLVFFVLAANNWCNLIPIVRWAFPYQTPDNHLMLLDVLCOLIYLL 372
Db :
QY 267 DMLFIQPRLOFVRGGDIIIVDSNELRKHYRTSKFOLDVASIIPDICVLYFGFPMFRAN 326
Db :
QY 373 DIITVFQRIQFVRGGDIIITDKEMRNYYKSFQXMDMLCLLPDLLLYLKFGVNPLLRP 432
Db :
QY 327 RMLKYTSFFEFNHLESIMDKAYIVRVIRTGTGYLLFILHINACVYVNASVEGIGTTREW 386
Db :
QY 433 RCLKYMAFEFNNRLESILSKAYVYVIRTAVALYSLHNSCLYMASAVEGLGSTHWV 492
Db :
QY 387 YDGEGNEYRCYVNAVRTLIITGCLPEOTLFEIYPOLLNFPSGVFVSSLIQGRDVIG 446
Db :
QY 493 YDGVGNSYRCYVNAVKTLITIGLDPRTLFEIYFQGLNYFTGFVAFSVMIGMRDVYG 552
Db :
QY 447 AATAQNYPFRACMDDTIAYMNYSIPKLQKRVRTWYETWDSQRMLDESLLTKLTPTTV 506
Db :
QY 553 AATAGQTYRSQMDSTVKYNFYKI PRSQNRVKTWYETHISQGMDESELAWQLPDQM 612
Db :
QY 507 QLALAIDVNFISIISKVDLKFQCDTOMIDMLRLKSLVYLPDGFVCKKGKEIKENYIKH 566
Db :
QY 613 RLDAIDVNSYISVKVALLFOGCDROMIFDMALKRLSVVYLPNDYVCKKGEIGREMYIIQA 672
Db :
QY 567 GEVOVLGGPDGTAVTLTKAGSVFGEISLLAAGGNRRNTANVAVGFANLLTKKTLQE 626
Db :
QY 673 GOVOVLGGPDGKSVLTVLTKAGSVFGEISLLAAGGNRRNTANVAVGFANLLTKKTLQE 732
Db :
QY 627 ILVHPDSEBRLMKCARVLLIQAKTAEAATPPRKQIALLPKKEBTPLFKTLTGCTGA 686
Db :
QY 733 ILVHPESQKLKARRMLRNKK-----PREKSVLILPRAAGTPKPLFNAALAAAGM 786
Db :
QY 687 SL-----ARLLKLRQAOKKENSEGGEKEKEDKOKENEDKQENEDKG 734
Db :
QY 787 GAXGGRGRIALLRALKELAALAAAROOL---LEQAKSEDAAVGE-----G 834
Db :
QY 735 KENEDKQGEPEEKPLDRPECTA-----SPIAVEEPEHSVRTVLP 776
Db :
QY 835 SASPEQPRPEPAPAPAPEPTAPFLAPEAPAPASPSPPPASQSPGSDXAARP 894
Db :
QY 777 RGTSROSLIISMAPSABGGEVUTIEVKEKAKQ 809
Db :
QY 895 ---EEHFVRHVITLGPDPSEQILLVEPEKQEE 924

RESULT 12
O77660 PRELIMINARY; PRT; 952 AA.
ID O77660
AC O77660;

```
Db 617 RDLDAIDVNSIVSKVALFQCDSQFMFLKRLRSVYVLPNDYVCKGIGREMIQIA 676
Qy 567 GEVQVLGPDGDTKVLVILKAGSVGEISLLAAGGNRTANVVAHGPANLLTLDKTKLQE 626
Db 677 GQVQVLGPDGDKSVLVLKAGSVGEISLLAAGGNRTANVVAHGPANLLTLDKTKDNE 736
Qy 627 ILVHYPSERILMKKARVLLKOKAKTAEATPPRKDLALLPPKEETPKLFTKLLGGTGA 686
Db 737 ILVHYPSQKLRLKARMLNNK-----PKSKVLIILPPRAGTPKLFNAALAAAGM 790
Qy 687 SL-----ARLLKIKREQAQKXENSEGEEGKEDKQKEDKQKEDK 734
Db 791 GAKGGRGRLALLRLKELAAEAARQQOL---LEQAKSSEDAVGE-----G 838
Qy 735 KENEDKQKREPEEKPLDRECTA-----SPLAVEEPHVSVRTVLP 776
Db 839 SASPEQPPRPPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 898
Qy 777 RGTSRQSLITSMAPSARGBEVITIEYKKAQ 809
Db 899 --BEHVRVHVLGPPSPQILLVVEPEKQEE 928

RESULT 13
Q9W2D5 PRELIMINARY; PRT; 1037 AA.
AC Q9W2D5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE CG17922 protein.
GN CG17922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattie B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
```

```
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003454; AAF46752.1; .
DR FlyBase; FBgn0034656; CG17922.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K_channel_pore.
DR Pfam; PF00027; CNMP_binding_1.
DR Pfam; PF00520; Ion_trans_1.
DR SMART; SM00100; CNMP_1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS00842; CNMP_BINDING_3; 1.
KW Ionic channel; transmembrane.
SQ SEQUENCE 1037 AA; 118393 MW; FCFB7A1590E7F051 CRC64;

Query Match 26.1%; Score 1103; Length 1037;
Best Local Similarity 33.4%; Pred. No. 1.1e-68;
Matches 243; Conservative 153; Mismatches 255; Indels 76; Gaps 13;

Qy 16 ENNEEQSRNEEGSHPSNOSQOTTAQ-----EENKGEKSLKTSPTVTSEPTNI 69
Db 276 EEEEEKSLHVESQPDVDEQDVQICYNSEFELQNEEDRNETQRTQTSINESEIVAV 335
Qy 70 QDKLSKNSGDLTNPDPQNAEPTGTVPQEKMDPKGKSPNQKPPAAPVINEYAD 129
Db 336 DEPTENMSVD---HRKPSA---GSLDSQGG-----QFLR 366
Qy 130 AQLHNLVKRMPQRTALYKCKLVEGDLSSPEASPTAKPTAVPVKESDDKPTHEYALLW 169
Db 367 DQVRHLVRRFTARANKVKRSI---ELPPTSSSTSVSPPTKSLHSP-QH----- 416
Qy 190 FKVKKMPLEVLKRIK-----PNSIDSYTD---RLYLLMLLTLA 228
Db 417 -KVLVFPAGQPHRGLFEADTPRSNWLSCGANDERTLDPQKRIYISLVCVVSLS 475
Qy 229 YNNWCWFIPLRLVFPYQTADNIHYWLIADICDIYLYDMLFQPRLOFVRGGDIIVDSN 288
Db 476 FLYNAWVPLRASFPPTKENTNLWACDFCADIIYLLDVVFFKRVWYLFEGFWKQKN 535
Qy 289 ELRKHYSITSKFQLDVASIIPFDICYLFFGFENPWF-PANRMLKYTSFFFNHLESIMDK 347
Db 536 LTRKXYNRKQKQKDLALLLELLYFKLGTAQVWLRFPPFKIQSFWEVRLDRVSS 595
Qy 348 AYIYRVIRTTGLYLFIHINACVYVWASNYEGIGTTRWYVDGEGNEYLRYVWAVRTLI 407
Db 596 PHFVRVAKTLTYMLYMIHITAAIYAYSDYQGLQGNWVFGKHGHPVRCFAATKATS 655
Qy 408 IGLPPEQTLPEIVQQLNFFSGVFFPSLIGQVRDVIGANTANQNFVFRACMDDTIAYMN 467
Db 656 IGKPKPERQGEYVFMVAVMLGMGVFALLIGQIRDIISTATNKHGYRQLEDELEYMR 715
Qy 468 NYSIPKLVQKVRVTWYTYTWDOSRMIDESLLKTLPTTVOLALADVNFISIISKVDLFG 527
Db 716 RLNLSEVQSRVWVWFQTEQRTLDSENLALPALPNLKTDAISVHICTLSKVQLFAD 775
Qy 528 CDTQMIVDMLRLKSVLYLPDGFVCKKGIGKEMYIKHGEVQVLGPGDTKVLVTLKAG 587
Db 776 CEEALLRDLVLRVAVTFLPDGFVCKRGEVREMYIVKLQGVQVMGSPSDVYVLAFLTEG 835
Qy 588 SVFGEISLLAAGGNRTANVVAHGPANLLTLDKTKLQETLVHPDSEIRILMKKARVLL- 646
Db 836 SVFGEISLLGINGADRRTADVRSKGSNLFVLSKSDNLNEIAYIPTAQAILKGRQLMR 895
```

647 KOKAKTAEATPRKDLAL-----LPPPK--EETPKLTKLLGGTGKASLAEKLLKKEQA 699
896 KNAAREEEREERARSALQADVIGNPKTPETAPKLTQVIQALPFPSPAVLITRSKR 955
700 AOKKENS 706
956 MRKRQS 962
PRELIMINARY; PRT; 1040 AA.
Q8IH43
AC Q8IH43
DT 01-WAR-2003 (TREMELrel. 23, Created)
DT 01-WAR-2003 (TREMELrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE GH25102p.
GN CG17922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreesen D., Farfan D., Frise E.,
RA George S., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo K.J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT001439; AAN71194.1; -.
DR FlyBase; Fgn0034656; CG17922.
DR GO; GO:0016020; Cmembrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; CNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel pore.
DR Pfam; PF00027; CNMP binding; 1.
DR Pfam; PF00520; ion trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP BINDING_1; 1.
DR PROSITE; PS00889; CNMP BINDING_2; 1.
DR PROSITE; PS00042; CNMP BINDING_3; 1.
DR PROSITE; PS00042; CNMP BINDING_3; 1.
SQ SEQUENCE 1040 AA; 118713 MW; 44643FDA21D2D5B8 CRC64;
Query Match 26.1%; Score 1103; DB 5; Length 1040;
Best Local Similarity 33.4%; Pred. No. 1.2e-68;
Matches 243; Conservative 153; Mismatches 255; Indels 76; Gaps 13;
Qy 16 ENNEOSSRRNEGSHPSNCQQTAAQ-----BENKGEKSLKNTSTVTEEPHTNI 69
Db 279 EEEEEKSSPLHVESQPDVDEQDVQICYNESPELQNEEDRERTQRTPSINESIVAV 338
Qy 70 QDKLSKNSGDLTTPDQNAAREPTGTVEPEQKEMDFGKGPNSQNKPPAPVINEYAD 129
Db 339 DEPTENMSVDV---HRKPSSA---GSLDSQGG-----QFLR 369
Qy 130 AOLNLVKRMQRALYKKLVGDLSSPEASQTAFTAVPPVKESDDKPTSHVYVLLW 189
Db 370 DQVRLVRRFTARANKVKSRI---ELPFTPSSTVSSPPTKSLHPSF-QH----- 419
Qy 190 FKVKMPLTEYLKRIKL-----PNSIDSYTD---RLYLLMLLLVTLA 228
Db 420 -KVLVFAQSPHGRFLFEADTPRSNVLCSLGCANNDERTLDPQGIYISMLCVVSL 478
Qy 229 YNWCNWFIPFLVFPYOTADNIHYWLIADIICDIYLYDMLFQPLQFVRGGDIIVDSN 288

Db 479 FLYNAWVIFLRASFPQTAKENTINWACDFCADIIYLLDVFVKHVMYLFEGFWKKN 538
Qy 289 ELKHKVTRTKFOLDVASIIPFDICYLFFGFNPMF-RANRMLKYTSTFFFNHLESIMDK 347
Db 539 LTRKNYRKLOFKLDLALLLELLYFKLGTQAVMLRPFPRFKIQSEWVFRLLDRVISS 598
Qy 348 AYIYRVIRTTGYLLFILHINACVYWNASVBEIGTTRWVDGEGEYLCYKVAVTLLIT 407
Db 599 PHEVRVAKTLTYMLYMIHTAALYYAYSQYQGLQNRWVFGKGGHYVRCFAFATKATS 658
Qy 408 IGGLEPOTLFEIVFQLLNFFSGVFFVSSLIQMDRVDVGAATANQNYFRACMDDTIAYVN 467
Db 659 IGKNPKEGCEYVFTVAVLMGVFALLIGQIRDIISTATRNKHEYROLEDETELEYMR 718
Qy 468 NYSIPKLAVQKRVRYEYTWDSQRMILDESLLKTLPTTTLVOLALAIQVNSIISKVLFGK 527
Db 719 RLNLSEQVQSRVQWFOFTWEQQRTLDSENLDPALPINKTKTIAISVHIQTLSSKVLQFAD 778
Qy 528 CDTOMIYDMLLRKSLVLYLPGDFVCKGKGEKEMYLKKGGEVQVVGSPDCTKVLVTLKAG 587
Db 779 CEEALLRDLVLKURAVTTFPGDFVCRKGEVREMYIVKLQVQVGMGPFSSDVLATLLEG 838
Qy 588 SVFGEISLLAAGGGRRTANVAHGFANLLTLDKKTLOEILVHYHPDSEILMKKARVLL- 646
Db 839 SVFGEISLLGNGADRTADVRSKGSNLFVLSKSLDNEVIAYYPTAAILKRRAROLMR 898
Qy 647 KOKAKTAEATPRKDLAL-----LPPPK--EETPKLTKLLGGTGKASLAEKLLKKEQA 699
Db 899 KNAAREEEREERARSALQADVIGNPKTPETAPKLTQVIQALPFPSPAVLITRSKR 958
Qy 700 AOKKENS 706
Db 959 MRKRQS 965
PRELIMINARY; PRT; 800 AA.
P90975
AC P90975
DT 01-MAY-1997 (TREMELrel. 03, Created)
DT 01-MAY-1997 (TREMELrel. 03, Last sequence update)
DE 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Cyclic nucleotide-gated channel.
GN P36P2.5 OR TAX-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97048185; PubMed=8893026;
RA Coburn C.M., Bargmann C.I.;
RT "A putative cyclic nucleotide-gated channel is required for sensory
development and function in C. elegans.",
RL Neuron 17:695-706(1996).
DR EMBL; U73476; AAB41492.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR000595; CNMP binding.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K+channel pore.
DR InterPro; IPR001202; WW_Rsp5 WWP.
DR Pfam; PF00027; CNMP binding; 1.
DR Pfam; PF00520; ion trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP BINDING_1; 1.
DR PROSITE; PS00889; CNMP BINDING_2; 1.
DR PROSITE; PS00042; CNMP BINDING_3; 1.
DR PROSITE; PS00159; WW_DOMAIN_1; 1.

KW	Ionc channel; Transmembrane.	
SQ	SEQUENCE 800 AA; 92462 MW; D0498AD2C340FDAA CRC64;	
	Query Match 25.9%; Score 1096; DB 5; Length 800;	
	Best Local Similarity 31.5%; Pred. No. 2.5e-68;	
	Matches 253; Conservative 146; Mismatches 301; Indels 102; Gaps 19;	
QY	26 RNEGSHPSNQSQQTTAAQENKG-----EESKLTKSTPTVTSSEPHNTNIQDKLSKQSSG 80	172
Db	17 RKREFSYVDROKASKPTQLSEKWKWSPRSEDSFLLDPANASKEP----- 61	
QY	81 DLTTNPPQNAAP-----TGTVPRQKE-----VDPKGEPSNQNPQPA 120	
Db	62 SASRFLPYPTPTPEVVIQIDEVESFILGLIDETDDELDGRDLDPASSFDSATSLSATRA 121	
QY	121 APVINEYADAQ-----LHNLVKRMQRQTALYKKKLVEGLSSPEASPTAKPTAVPP 172	
Db	122 SSIIEDDVRSQISFIMRERLHSAKEVHRRTSAVREDLIR---ETPEDTVSMA--SNVP- 175	
QY	173 VKESDDKPTHEYHLLMKPKV-KWPLTEYLKR-----IKLPNSIDSYTDRLYLLMLLVTLA 228	
Db	176 -KQNEHPS--LMSLIGLQNRSESPYTDVTKNCFGSLKGTFFPY-GRFYMTLWLSVTL 231	
QY	229 YNNMCWPIRLRVFPYQADNIHWLMTADIIICDIYLYDMLFTQPRLOFVRGGDIIVDSN 288	
Db	232 FLNFAICIPLRSSPYQADNMWFIIVDYSCDLVYVIDMLLIKPLRFLTRGGIQVKIYK 291	
QY	289 ELKXHYRTSKFQLDVASIIPFICILYFFGFNPMFRANMLKYTSPFEFNHLESIMDKA 348	
Db	292 DTQRHLYMTRTFKLDLSILPTD.LMYFFGCKPIWRINRVKINSFWLLFDMLDLSFANP 351	
QY	349 YIVRVITTCYLLFILHINACTVYMASNYEGIG-----TTRWYVDGEGNYLRC 397	
Db	352 YAIRIARTLSYMIYIHCNSCVYKLSALQAFQIAYLENGKWLKWKVYNNQGNAYIRC 411	
QY	398 YWAVRLLTIIGGLPEPQTFEIVFOLLNFFSGVVFSSLIGOMRDVIGAAATANYERA 457	
Db	412 FYTAAVATSTGNPAPTNVIEIYVTCSSWNGVVFALLGGIIRDIVSVANRRNEEF 471	
QY	458 CMDDTTAYMNNYSIPKLQVQRVTWZEYTWDSQRMLEDSDLLKTLPTTVQLALADVNF 517	
Db	472 KMDLALGECKGLGKMETTNVRDWFVFTYWOQOKTLDEKGLIEKLPLKQLTDLALSVHT 531	
QY	518 IISKVDLFFKCDTQMLYDMLLRKLSVLYLPDGVCKKGIGKEMYLIIKGEVQVLTGGPG 577	
Db	532 TLSKQVQFOCDRALLURDLKURPFIIFPGDMICLKGVDGKEMYIIINGIILQWGDHN 591	
QY	578 TKYLVTLKAGSVEGISLLAAGGNRRRTANVAHGFANLLTLDKKTQLRILVHPDSERI 637	
Db	592 EKIFAEALQAGVFEISLLAIGNNRRRTASIRAKGYCTTLFVLAKEDLNDVIRYYPQAFI 651	
QY	638 LMKARVLLKQAKTAAEATPPKDLAIL-----FPPKEETPKLFTLLGGT-----GKA 686	
Db	652 LRRKAAAMLKNDKKSDEKTEKIAQAALEDRCKINPR-QVPKLIITLIANNTEMNENKGVQ 710	
QY	687 SLARLLKLRQAAQKK-----ENSGEGEEGKENEDKOKENED-----KOKENED 732	
Db	711 ELKQVLEEETESRRRSIYYPNASTLQRDDDDDEEWNDEEDLSDVGEDFLDPTNHSDD 770	
QY	733 KOKENEDKQGREPEEKPDLRP 754	
Db	771 ---PWEDVDLAPEVHDDDDWQDP 789	

Search completed: June 21, 2004, 10:07:18
Job time : 57 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 10:04:22 ; Search time 21 Seconds
(without alignments)

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSLTKVNVKVPIGENNEN.....PSAEGGSEVLTIETVEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100

Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

```
2: pir2:~
```

3: p1r3:

4: p1r4:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	1952	46.1	909	S32538	CGMP-gated cation
2	1095	25.9	800	T19627	hypothetical prote
3	834.5	19.7	695	S74179	cyclic nucleotide-
4	829	19.6	663	S11521	CAMP-gated channel
5	821.5	19.4	735	S10630	alpha subunit of c
6	820	19.4	732	S35691	cyclic nucleotide-
7	819.5	19.4	688	E41261	CGMP-gated cation
8	818.5	19.3	690	A41261	CGMP-gated cation
9	818	19.3	686	A44842	CGMP-gated ion cha
10	807.5	19.1	682	JH0560	cyclic nucleotide-
11	804	19.0	664	S11517	cyclic nucleotide-
12	801.5	18.9	691	S05103	rod cyclic nucleot
13	797	18.8	690	JC7909	CGMP-gated ion cha
14	794	18.8	706	A55251	cyclic nucleotide-
15	771	18.2	645	S36680	alpha subunit of r
16	770	18.2	772	S28292	hypothetical prote
17	718	17.0	665	S52072	DMNCG protein - f
18	640	15.1	575	S19327	olfactory cyclic n
19	555	13.1	673	T20936	hypothetical prote
20	530	12.5	611	T20935	hypothetical prote
21	484	11.4	261	T17859	cyclic nucleotide-
22	476	11.2	261	T178560	cyclic nucleotide-
23	441.5	10.4	644	T31125	hypothetical prote
24	366.5	8.7	767	T21969	hypothetical prote
25	349	8.2	828	T52046	potassium channel
26	339	8.2	962	T53197	potassium channel
27	336	7.9	989	T14912	potassium channel
28	331.5	7.8	807	T12177	potassium channel
29	323.5	7.6	845	T07052	probable potassium

ALIGNMENTS

RESULT 1

532538

cGMP-gated cation channel 2, rod - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 16-Jul-1999

C;Accession: S32538

R;Chen, T.Y.; Peng, Y.W.; Dhallan, R.S.; Ahamed, B.; Reed, R.R.; Yau, K.W.

Nature 362, 764-767, 1993

A;Title: A new subunit of the cyclic nucleotide-gated cation channel in retinal rods.

A;Reference number: S32538; MUID:93226050; PMID:7682292

A;Accession: S32538

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-909 <CHE>

C; Superfamily: cAMP receptor protein cyclic nucleotide-binding domain homology

C;Keywords: cGMP binding

F;620-742/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match	46.1%	Score 1952	DB 2	Length 909
-------------	-------	------------	------	------------

Best Local Similarity 46.4%; Pred. No. 5.4e-112;

Matches 405; Conservative 121; Mismatches 237; Indels 110; Gaps 18;

[illegible]

```

Db 477 GSTHWVGVGNSYRCYFAVKTLLITIGLPDPKTLFEIIVFQLLNYFTGVFAFSVMIGQ 536
QY 441 MRDVI GAATANQYPRACMDDTIANNYSIPKLVOKRVRTWYETWDSQRLMDESLLK 500
Db 537 MRDVVGAATAGQTYRSCWDSVTVMNFYKIPKSVQNRVKTWYETWHSQGLMDESILMV 596
QY 501 TLPTTVQALALADNVFSIISKVLDFKGDCTOMIVDMLRLKSLVLPDGFVCKGEIGKE 560
Db 597 QLPDNRDLALDVNNYIVSKVALFQGDQRMIFDMLKRLSVVLVNDYVCKGEIGRE 656
QY 561 MYIIKHGEVQVGLGGPGDKVLVTLKAGSVFGEISILAAAGGNRRRTANVAHFANLLTLD 620
Db 657 MYIIQAGVQVGLGGPGDKSLVTLKAGSVFGEISILAVGGNRRRTANVAHFANLLTLD 716
QY 621 KKTLOSILVHVPDSERIILMKARVLLKQAKTAETAPRKDLALFPKKEETPKLKTLL 680
Db 717 KIDLNEILVHVPESOKLURKARRMLRNNK-----PKKEKSVLILPPRAGTPKLFNAAL 771
QY 681 GGTGRAS-----LAKLLKREQAQKENSEGEGEECKENEDKQK 728
Db 772 AMTGRMGKGAGKGLAHLARLKLALALEAAKQOEL---VEQAKSSQDVKGEGSAAP 828
QY 729 ENEDKGKE-NEDKXGRPEKPEP-----LDRECTASPIAVEEPHPSVRTVLP 776
Db 829 DQHTHPKEAATDPPAPRTPPEPFGSPSPSPASLGRPEGEEGPA-EPEHSHVR----- 882
QY 777 RGTSRQSLIISMAPSAGEEVEVLTIEVKEKAKQ 809
Db 883 -----ICMSPGPEGEQILSVKMPERE 906

RESULT 2
T19627
Hypothetical protein F36F2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T19627; 121863
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19627
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-800 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07847.1; GSPDB:GN00019; CESP:F36F2.5
A:Experimental source: clone C31H5
R:Cottage, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19479
A:Accession: T21863
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-800 <W12>
A:Cross-references: EMBL:Z81532; PIDN:CAB04328.1; GSPDB:GN00019; CESP:F36F2.5
A:Experimental source: clone F36F2
C:Genetics:
A:Gene: CESP:F36F2.5
A:Map position: 1
A:Introns: 27/3; 51/2; 142/2; 191/3; 287/3; 333/3; 355/2; 405/1; 433/2; 484/1; 508/1; 56
Query Match 25.9%; Score 1095; DB 2; Length 800;
Best Local Similarity 31.9%; Pred. No. 1.9e-59;
Matches 258; Conservative 153; Mismatches 301; Indels 98; Gaps 22;
QY 2 FKSLLTKVNVKPIGNNENNEOSSRNEG-----SHPSVQSQTAAQENKGEESLTKYST 58
Db 21 FSYVDKQKASRPT-QLSEKWKSPRSDSFDLLDPANAS-----KEPSASTRPL 68
QY 59 PV-TSEEPHTIQDKLSKKNSSGDIITNP-----DPQNAEPTGTVPQEKMDPGKEGPN 112
Db 69 PYPPTRPPEVVIQI-----DEVESPIGLIDETDDHLDG-----RLDPASSFDA 113
QY 113 SPQNKPPAAPVINEYADAQ-----LHNLVKVRORTALYKKKLVGDLSSPEASPT 164

```

```

Db 114 NSLSATRASIIEDDVRSQISFIMBERLHSAKEVHRTISAVREDLIR---ETPDTVSM 170
QY 165 AKPTAVPPVKESDDKPTHEYRLLMFKVK-KMPLTEYLKR---IKLPSIDSYTDRLYLL 220
Db 171 A--SNVP--KQNEHRPS--LMSLIGLQNRSEPTVDTKNCFGSLKGTFFPY-GRFYNT 223
QY 221 WLLLVTLAYNNMCWFTPIRLVFPYOTADNIHFWLADIICDIILYDMLFTQPRLOQVRG 280
Db 224 WLSVLTCLFNAFCIPLRSSPYQTDANNMTWFIYDSCDLYVIDMLLKPRFRTRG 283
QY 281 GDIIVDSNLRKHRTSTRTKFQDVASIIIPDFICYLFFGFNPMFRANRLKTSFFEFNHH 340
Db 284 GIQVKIYKDTQRHYLMTRTFKLDLSILPTDLMYFFFGKPIWRINRVLKINSFWLLPDM 343
QY 341 LSSIMDKAIYVIRVTGTYLLFILHINACVYVWASNYEGIG-----TTBWYVDG 389
Db 344 LNSFANPAIRIARTLSYMIYIIHCNSCVYKLSALQAFQGIAYLENGKWYLNKWVYNN 403
QY 390 EGNEXLCRYWAVRTLITIGGLPEPQTLEIIVFQLLNFFSGVVFSSLIQMRDVIGAT 449
Db 404 QGNAYIRCIFYFTAATVATSGNNPAPTNIYVYMTCSWMMGVFVALLGQIRDIVSNAN 463
QY 450 ANQNYPRACMDDTIANNYSIPKLVOKRVRTWYETWDSQRLMDESLLKTLPTVQLA 509
Db 464 RNREEFQRMDLALGECKKLGKMETTNVRDMFTYTQOQKTLDEKLEIKLPLQTD 523
QY 510 LAIDVNFSTIISKVDLPFKGCDTOMIVDMLRLKSLVLPDGFVCKGEIGKEMVYIKHGEV 569
Db 524 LALSVMHTLSKVQLFQDCDRALLDLVLKRPVLPFDGMLCLKSGDVKEMVYINQOIL 583
QY 570 QVLGGPDGTVLTVTLKAGSVFGEISILAAAGGNRRRTANVAHFANLLTLDKKTLOEILV 629
Db 584 QVVGPDHNEKIFAELAQGAVFGEISILATGNNRRRTASTIRAKGYCTLFVLAKEDLNDVIR 643
QY 630 HYPDSERILMKARVLLKQAKTAETAPRKDLALL-----PPKKEETPKLTKLGGT- 683
Db 644 YTPQAOITLRRKAAAWLKNDKSDKTEKIKQAQAELEDRCNKINPR-QVPKLITLITANMTE 702
QY 684 -----GKASLARILKLRQAAQK-----ENSEGEEEGEKENEDKQKENE- 725
Db 703 MNENKGVQELKKVIBETEKSRRQIYVYVPSWTSLQDDDDDEEWDEEDLSVGDGFDLDP 762
QY 726 -KQENEDKCKENEDKCKGPEPEKPLDRP 754
Db 763 TNHSDDED---PMEDVDVLAPEVHDDDDQDP 789

RESULT 3
S74179
Cyclic nucleotide-gated channel protein - human
C:Species: Homo sapiens (man)
C>Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999
C:Accession: S74179
R:Yu, W.P.; Grunwald, M.E.; Yau, K.W.
FEBS Lett. 393, 211-215, 1996
A>Title: Molecular cloning, functional expression and chromosomal localization of a human
A:Reference number: S74179; MUID:96409310; PMID:8814292
A:Accession: S74179
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-695 <YUW>
A:Experimental source: retina
C:Genetics:
A:Superfamily: 2
A:Map position: 2
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: ion channel; ion transport; membrane protein
F:482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 19.7%; Score 834.5; DB 2; Length 695;
Best Local Similarity 29.7%; Pred. No. 1.5e-43;
Matches 223; Conservative 149; Mismatches 271; Indels 107; Gaps 22;

```

```

27 NEBSGHSNOSQQTAAQENKGEBSLTKTSPTVTEEPHTNIQDKLSKNNSCDLITNP 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
5 NTOYSHPS-----RTELVKTTSDRLNRAENGSLRAHSSEETS-- 43
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
87 DPONAABPTGTVPEOKEMDPCKECPNSPQNKPPAAPVINEYADAQLHNLVKRMQRTALY 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
44 ---SVLOP-GIAMESTRGLADSGGGSFTGO-----GIARSLRILFLRRWAARH 87
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
147 KKKLVBGDLSP-----EASPTAKTATVPVVKESDDKTEHYRLLWFKVKMPL 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
88 VHHQDQGFDPDFRGAELKEVSSQESNAQANVGSOEPADRG-----ESAW-----PL 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
198 -----TEYLKRIKLPSNI-DSVTDRLYLWLLWLLVTLAYNWNWCWFPLRLVPYQOT 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
137 AKCNTNTSNITEBEKTKKDAIVVDSPSSNLYRRLTAIALPVFYNWYLLICRACFDELQ 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
247 ADNIHYWLIADIIICDIYLVDMFIQPRLOFVRGGDIIIVDSNELRKHRYRTSTKFOLDVAS 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
197 SEVLMMLVLVDYSADVLYLDVL-VRAARTGFLSQGLMSDTNRLWQHYKTTTQFKLDVLS 255
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
307 IIPEDI CVLPFGFN-PMFRANRMLKTYSPFEFNHLESIMDKAYIVRVIRTTGYLLFILH 365
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 LVPTDLAYLVKGTNYPEVRFNRLKPSRLFEFPDRETETRYNPMFIGNLVLYLIIH 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
366 INACVYWASNYEGIGTRWYVDG-----BONEYLCYVYAVRVLTIITIGGLPEPQTL 417
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
316 WNACIYPAISKFIFGFGTSDWYPYNISIPERGLRSKRYISLYMSTLTLTIGETPPVKD 375
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
418 PEIVFOLLNPFSGVVFSSLLIGQMRDVI GAATANONVFRACMDDTIAYMNNYISIPKLVOK 477
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
376 EYLVFVVDFLVGLVLIIFATIVGNVGSIMSNNASRAEFOAKIDSIKYMQFRKVTKDLET 435
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
478 RVRTWYBTWDSQRMLESDDLKTLPTTVQALAIADVNFISIISKVLFGCDTQMIVDML 537
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
436 RVIRWFYDLWANKVTBDEKVLKSLPKLKAETIAINHLDTLKKVIRFOCEAGLIVELY 495
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
538 LRLKSVLVLPGDVFCCKGEICKEWYIIKHGBVQVLGGPDGFKVLVTLUKAGSVFGEISLLA 597
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
496 LKLRTVPSPGDYICKKGIDIKGEWYIINEGKLVV-ADDGVTQFVVLSDGSYFGEISILN 554
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
598 AGG---GNRRNTANYVAHGAFANLLTLDKKTLOEILVHYIP-DSEIRILMKKAR-VLLKQK--- 649
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
555 IKGSKSGNRRNTANIRSIGSYDLFCLSKODLMEALTEYPGQAKKALBEKGRQILMKONLID 614
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
650 AKTAEATPPRKDALLPPPKETPKLTKTLGGTGKASLARLL-----KLKRECAAQ 701
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
615 EELARAGADPKDL-----EBKVQLGSSL--DTLOTRFAKLLAEYVATQWKKQRLSQL 666
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
702 KKENSEGEE---EGKENEDKOKENEDKQK 728
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
667 ESQVKGGDGDKPLADGEVPGDATK-TEDKQO 695
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 4
S11521
cAMP-gated channel protein - bovine
C.Species: Bos primigenius taurus (cattle)
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C.Accession: S11521
R.Ludwig, J.; Margalit, T.; Eismann, E.; Lancet, D.; Kaupp, U.B.
FEBS Lett. 270, 24-29, 1990
A.Title: Primary structure of cAMP-gated channel from bovine olfactory epithelium.
A.Reference number: S11521; MUID:91032022; PMID:1699793
A.Accession: S11521
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-663 <LUD>
A.Cross-references: GS:X55010; NID:g287743; PID:g287744
C.Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
F:454-578/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match
Best Local Similarity 29.9%; DB 2; Length 663;
Pred. No. 3.1e-43;

```

	Matches	218; Conservative	132; Mismatches	283; Indels	96; Gaps	20;
Qy	50	EKSLTKSTPVTSEBPHNIQDKLKNSSGDLTTPDPONAA--BPTGTVPQEKEMDGP	107			
Db	3	EKANGVKSPPANNHHHAPPAIKASGD---DHRASSRPOSAADPTSSELQAELMADAP	59			
Qy	108	KEGENSPONKPPAAPVINEVA-----DAQLNLVKRMQRORTALYKKLVLEDGLSSPEA	160			
Db	60	QQRRGGFRRLARLVGLURWAYRNFRREBPPOSFLEFR-----GPEL	103			
Qy	161	SPTAKPTAVPPVKESDDKTEPHYRYLLMPKVKKMPLTEYLKRILKPNSIDSDTYDRLYLL	220			
Db	104	HTVTTQGCGDKDGSGKGTKKKFLF-----VLDPAGD-WYYR	142			
Qy	221	WLLIATLI--AYNNCNCFPIPLRVFPFYCTADNIIHWLIADIICDIIVLYDMLFIQPRLOQV	278			
Db	143	WLFIUAIPLVLYNN-CLLV-ARACFSDLQGYIIVWLVDVSUVVIAD-LFLERLTGPL	198			
Qy	279	RGGDIIIVDSNELRKHYSTSTKFOLDVASIIPFCICYLFFGF-NPMFANRLMKYTSPFEF	337			
Db	200	EOGLLVKDRTKLRDNYIHTMQFKLDVASIITPTDIIYFAVGITHNPVEVFNELLHFARMFEF	259			
Qy	338	NHHLESIMDKAIYVRVIRTTCYLLFILHIINACYVMASNVSEGIGTTRWVY----DGE---	390			
Db	260	PDRFETSTSPNIFRISNLIYLIITIIHNWACYIAYSKSIIGTGVDTWVTPNITDPGYG	319			
Qy	391	-GNELYLRCYMAVRTLITIGLPPEPOTLPFIVFOLLNFPSGVFVSSLIQOMRDVIGAAT	449			
Db	320	LSREVIYCLYWSTLTLTTIGETPPPVKDEEVLFPDFLIGVLIFATVGNVSMISNMN	379			
Qy	450	ANONYFRACMDDTIAYNNYSIPKLVOKRVRTWEYTWDSQMLEDSDLLKTPTTVOLA	509			
Db	380	ATRAEPQAKIDAVKHXYQFQKVKMEAKVIRPDFDYLTWKTKSVDEREVLKNLPKAKURAE	439			
Qy	510	LAIQVNFISIISKVDLPFGCDTQMIDYMLLRALKSVLYLPFGDVCKKGKIGKEMYIIKEGEV	569			
Db	440	IAINVHLSTLKVVRIPODCRAGLIVELVLKLRPQVFSPGDVICRGDYGKEMYIIKEGKL	499			
Qy	570	QVLGGPGTKVLTILKAGSVEFGSILSLAAG--GNERTANVAHGAFANILLTDKKTLOE	626			
Db	500	AVV-ADDGVTOYALLSAGSCFGEISILINIKGSXNGNRNTAIRISLGYSDFULCSDKDDLME	558			
Qy	627	ILVHPDSEIRILMKKAVLLKQAKTAEE--ATPPRKDALLLFPFKBEETPKLFTLLGGT	683			
Db	559	AVTEYPDRAKRVLEGRREILMKEGLLDENEAASMEVDV-----QEKLEQLETNW--DT	610			
Qy	684	GKASLARILLKLRQAAQKKENSSEGGEBEGKENEDKOKEN--EDQOXENEDKGENEDKD	741			
Db	611	LYTRFARLLL-----AYTGAQKKQRIITVLETKMRQNNEEDSLSDGMN	654			
Qy	742	KGRSPEEKP	750			
Db	655	SPEEPAEKP	663			
	RESULT	5				
		alpha subunit of cone photoreceptor CNG-channel - chicken				
		C.Species: Gallus gallus (chicken)				
		C.Date: 13-Sep-1996 #sequence_revision 13-Seg-1996 #text_change 13-Aug-1999				
		C.Accession: U50630				
		R.Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; X				
		Neuron 10, 865-877, 1993				
		A>Title: Rod and cone photoreceptor calls express distinct genes for cGMP-gated				
		A.Reference number: U50630; PMID:93264082; PMID:7684234				

RESULT 5

KE9071
I50630

alpha subunit of cone photoreceptor CNG-channel - chicken

atrial substrate of cone photoreceptors
C. macdonald, Callus calling (chicken)

C;Species: Gallus gallus (chicken)

C;Date: 13-Sep-1996

C;Accession: I50630

R; Bonigk, W.; Altenhofe

Neuron 10, 865-877, 1993

A;Title: Rod and cone photoreceptor cells express distinct

A: Reference number: I

A/Reference Number: T50630, MOID: 55204002, LMS: 70

A/Accession: T50630

A;Accession: 150630
 A;Status: preliminary

A;Status: preliminary;

A;Molecule type: mRNA

A;Residues: 1-735 <BON>

A;Cross-references: EMBL:X89598; NID:g908850; PIDN:CAA61757.1; PID:g908851

C; Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-


```

Db      3  LSKMTNIIINTWHSFVNI PNVIIPATEIKERIRRMENGACSFSDDDN-----GSLSESENE 57
Qy      106 PG-----KGGPNSPQKPAAPV---INAYADAQLHNLVKRMQRORTALYKKKLVEGD 154
Db      58  DSFFRSNYSKRGPSQREQLFETWALFNWNSSNKDQEPKPKKKKK-----EKSKKADD 113
Qy      155  LSPEASPOKTAFTAVPPVKESDKPTEHYRLLWPKVKMPLTEYLKRIKLPNSIDSYS 214
Db      114  KENKDKPEKKKKE---KEKPKKKE-----KTEKKEEBKKEVVVDPGNTVY 162
Qy      215  DRLLYLWLLVLT--AYNNCWPIPLRVPVQOTADNIHLYADIICDIIYLYDMFLQ 272
Db      163  N-----WLFCTILPVNMYNT--MIARACFDELQSDYLEWLFIDFVSNVYLAQM-FVR 214
Qy      273  PRLOFVRGGDIIVDSNELKHYRTSKFOLDVASIIPFDICYLFFGFN-PMFRANRMLKY 331
Db      215  TRTGYLEQGLLVKDRWKLIEKYKANLOFKLVDLSVPTDLYIKFGWNYPEIRLNELLRI 274
Qy      332  TSPFEFNHLESIMDKAYIRVIRTGTYLLFILHINACVYVWASNYEGIGTRWVY---- 387
Db      275  SRMFEFFQRTETRTNPNIFRISNLVMIYIIHWNACVYSISKALFGNDTWVYPDVN 334
Qy      388  DGE-----GNEYLCRYKAWRTLATIGLPEPQTLFEIVFOLLNFFSGVFSSLGOMED 443
Db      335  DPFGRLARKYVSLWSTLTLTIGETPPVLDSEVIFVVDVFLIGVLIFATVGNIGS 394
Qy      444  VIGAATANQNYFRACMDDDTIAYNNYSIPKLQKRVRTWYETWDSQRMLEDSDLLKTL 503
Db      395  MISNMNARAEFOSRDVAIKQYFNFRNVSKDMKRVLKWFDYLTWNTKTVDEREVLRLP 454
Qy      504  TTVOLALAIIDVNFISIKVDLFGKCDTQMIYDMLRLKSVLYLPGFVCKKGIGKEMKI 563
Db      455  DKLRAETAINVHLDLTKKVRIFADCEAGLLVELVLQPOVYSPGDYICKGDIKREMI 514
Qy      564  IKHGEVOVLGGPGDKTVLVITLKAGSVFGEISLLAAGG---GNERTANVAHGPFANLL 620
Db      515  IKEGKLVV-ADGGITQFVVLSDGSGFGEISILNIGSKAGNRTANIKSIGVSDLFCLS 573
Qy      621  KXTLQELVHYPPSERILMKARVLL 646
Db      574  KODLMEVLTEYPAKTMLEBKRGQIL 599

RESULT 8
A42161
CGMP-gated cation channel, rod photoreceptor - human
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999
C:Accession: A42161
R:Pittler, S.J.; Lee, A.K.; Altherr, M.R.; Howard, T.A.; Seldin, M.F.; Hurwitz, R.L.; Wa
J. Biol. Chem. 267, 6257-6262, 1992
A:Title: Primary structure and chromosomal localization of human and mouse rod photorece
A:Reference number: A42161; MUID:92210603; PMID:1372902
C:Accession: A42161
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-690 <P>
A:Cross-references: GB:M84741; NID:G180461; PIDN:AA52010.1; PID:G180462
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: cAMP binding; transmembrane protein
F:479-603/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match          19.3%; Score 818.5; DB 2; Length 690;
Best Local Similarity 30.0%; Pred. No. 1.5e-42;
Matches 221; Conservative 128; Mismatches 262; Indels 125; Gaps 22;

Qy      5  LTKVNVKXPIGNNENEGSSRRNEGSHPS-----NQSQQTAAQENKGE-----KSL 53
Db      17  VTMPNVIVP-----DIEKIRRMENGACSFSDDDSDAYTSESEENPHARGSFYSKSL 71
Qy      54  KTKSTPTVSEPHNTIQDKLKNSSGDLTTNPDPQNAABPTGVPSQKEMDPCKEGPNS 113
Db      72  R-KGGFSQREQLPGAIAIFNVNNS-----NKD-----QEPPEKKKKKKKKSKSDKNE 121

```

RESULT 9

```

A44842
CGMP-Gated ion channel protein - human
N:Alternate names: rod photoreceptor cGMP-gated channel
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A44842
R:Dhallan, R.S.; Macke, J.P.; Eddy, R.L.; Shows, T.B.; Reed, R.R.; Yau, K.W.; Nathans, J
J. Neurosci. 12, 3248-3256, 1992
A:Title: Human rod photoreceptor cGMP-gated channel: amino acid sequence, gene structure,
A:Reference number: A44842; MUID:92356211; PMID:1379636
C:Accession: A44842
A:Molecule type: mRNA
A:Residues: 1-666 <DHA>
A:Cross-references: GB:S42457; NID:G252853; PIDN:AAE22778.1; PID:G252854
A:Experimental source: retina
A:Note: sequence extracted from NCBI backbone (NCBI:110250, NCBI:110251)
C:Genetics:
A:Gene: GDB:CNCG1: CNCG
A:Cross-references: GDB:127557; OMIM:123825
A:Map position: 4p14-q4l3
A:Introns: 36/2; 75/2; 95/2; 110/2; 146/2; 182/2; 218/2
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: cAMP binding; eye; ion channel; ion transport; retina; transmembrane protein
F:475-599/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

```

```

Qy      114  POKPPAAPVINEYADAQLHNLVKRMQRORTALYKKKLVEGDLSPSEASPOKTAFTAVPPV 173
Db      122  NKNDPE-----KKKKKDKKKKK-----E 141
Qy      174  KESDDKTEHYRLLWPKVKMPLTEYLKRIKLPNSIDSYSYTDRLYLWLLVLT--AYNN 231
Db      142  ESKDKKEHH-----KKEVVV-----IDP-SGNTYYNWLFCITILPVNWNW 180
Qy      232  NCWFIPRLRVFPYQOTADNIHLYADIICDIIYLYDMFLIOPRLQFVRGGDIIVDSNELR 291
Db      181  T--WVIAACFDELQSDYLEWLLILDVSDIVYLDIM-FVTRTRTGYLEQGLLVKEELKI 237
Qy      292  KHYTSTKFDQDVASIIIPFDICYLFFGFN-PMFRANRMLKYTSPEFNHLESIMDKAYI 350
Db      238  NKYSNLQFKLVDLSIPTDLYIKFGWNYPEIRLNELLRFRMPEFFQRTETRTNPN 297
Qy      351  YRVIRTTGTYLLFILHINACVYVWASNYEGIGTRWVY----DGE-----GNEYLCRYWAV 402
Db      298  FRISNLVMIYIIHWNACVYSISKALFGNDTWVYPDINDPFGRLARKVYVSLYWS 357
Qy      403  RTLITIGLPEPQTLFEIVFOLLNFFSGVFSSLGOMRDVIGAAATANQNYFRACMD 462
Db      358  LTLTIGETPPVLDSEVIFVVDVFLIGVLIFATVGNIGSMISNMNARAEFQARIDAI 417
Qy      463  IAYNNYSIPKLQKRVRTWYETWDSQRMLEDSDLLKTLPTTVQLALAIIDVNFISIKV 522
Db      418  KOYMEFRNVSKDMKRVLKWFDYLTWNTKTVDEKEVLKYLDPKRAETAINVHLDLTKV 477
Qy      523  DLFGKCDTQMIYDMLRLKSVLYLPGFVCKKGIGKEMKIYKHGEVOVLGGPGDKTVLV 582
Db      478  RIFADCEAGLLVELVLQPOVYSPGDYICKGDIKREMIYKEGKLVV-ADGGITQFV 536
Qy      583  TLKAGSVFGEISLLAAGG---GNERTANVAHGPFANLLTLDKKTQELVHYPPSERIL 639
Db      537  VLSDGSTGGEISILNIGSKAGNRTANIKSIGVSDLFCLSKDDLMLEALTEYPAKTM 596
Qy      640  KKAARVLLKQKA---KTAEATPPRKDLALLPFPKPEETPKLFTKLGGTGKASLAE 692
Db      597  EKGKILMKDGLDLNLANAGSDPKLEEKVTRMEGSDVLLQT-----RFAIILAEY 648
Qy      693  -----KLKREOAQKK 703
Db      649  ESMQKQLKQRLTKVEK 664

```

Query Match 19.3%; Score 818; DB 1; Length 686;
 Best Local Similarity 29.3%; Pred. No. 1.6e-42;
 Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

QY 5 LTKAVKPKFIGNENEGSHPS-----NQSQTTAENKGE-----KSL 53
 Db 13 VTMNVIVP-----DIKXIRWENGACSSPESDDSDASTSESENPHARGSFYSKL 67
 QY 54 KTKSPVISEPHTHIQDKLKNKSGDLTPNDPQNAABPTGVPEKEMDPKQEGNS 113
 Db 68 R-KGSPSQEYLPQALFNVNNS-----NKK-----QEPKCKKKKKKSKSDKNKE 117
 QY 114 POKPAPAVINEYADALHNLVKKMRQRTALYKXKLVGDLSPSPQAKTAPVPPV 173
 Db 118 NKNDPE-----KXKKKKKKKK-----E 137
 QY 174 KESDDKPTHEYRLWFKVKQKMLTEYLKRIKLPNSIDSYTDRLYLWLLVTL--AYNW 231
 Db 138 EKSKDKKEE-----KKEVV-----IDP-SGNTYVNWLFCTITLPMVYNW 176
 QY 232 NCWFIPLRLVPYQADNIHYNWLIADIIIDYLDMLFIQPLQFVREGDIIIVDSNELR 291
 Db 177 T--MWIARACDFELQSDVLEWLIIDYSDIVLIDM-FVTRTGYLEOGLVKEELKI 233
 QY 292 KHYRTSTKPDVAGIIPFDICYFFGN-PMFANRMLKYSFPEFNHLESIMDKAYI 350
 Db 234 NKYSNLOKFLDVLISPTDLLYFKLGNWYPEIRLRLRPSRMFEPFQRTETRTNYPNI 293
 QY 351 YRVINTTGYLLFIHINACVYVWASNYEGIGTTRWVY-----DGE-----GREYLCYVWAV 402
 Db 294 FRISNLWYVIIHWNACVYSIKAKFGNDTWVVDINDPFGRLAKYVYSLYWS 353
 QY 403 RLITIGLPEPQTLFEIVFQLLNFFSGVVFSSLIQMRDVI GAATANQNYFRACMDT 462
 Db 354 LTLTIGETPPVRDSEYVVFVDFLIGLVIFATIVNIGNSMISNMNAARAEQARDAI 413
 QY 463 IAYNNYSIPKLVQKVRVTEYTWDSQRLMDESLKTLPTTQALAIADVNSISKV 522
 Db 414 KOYMHFRNVSKMEKRVIKFDYLTWNTKTVDKELKYLFDKLRARAIINVHLDLTKV 473
 QY 523 DLFGKCDQMIYDMLRLKSVLYLPQDFVCKKIGKEMVIIKHGEVQVVGDPGDKVLV 582
 Db 474 RIFADCEAGLAVELVQLQPVYSPGYCKKGLIGEMVIIKGLAVV-ADGVTOFV 532
 QY 593 TLKAGSVFGEISLLAAG--GNRRTANVAHGFANLTLTDKTLQELVHYPPSERILM 639
 Db 533 VLSGYSYFGEISILNIGSKAGNRTANIKSIGYSDIFCLSKDLMALTEYDPAKTMLE 592
 QY 640 KKAIVLLKQK-----KTAETPPKDLALLFPKPEETPKLTKLLGSGKASLARLL-- 692
 Db 593 EKGQILMKDGLDINTANAGSDPKLEEKVTRNEGSVDLLQ-----RPARILAEY 644
 QY 693 -----KLKREQAOKK-----ENSEG-GSEEG 713
 Db 645 ESMQCKLQRLTKVEXFKPLIDTFESSIEGPGAESG 681

RESULT 10

JH0560
 Cyclic nucleotide-gated channel - channel catfish
 C/Species: Ictalurus punctatus (channel catfish)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: JH0560
 R/Goulding, E.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Chess
 Neuron 8, 45-58, 1992
 A/Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated
 A/Reference number: JH0560; MUID:92110008; PMID:1370374
 A/Accession: JH0560
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-682 <GOU>
 A/Cross-references: GB:M8311
 A/Experimental source: Olfactory epithelium

C/Comment: This cyclic nucleotide-gated channel is activated equally well by both cAMP and cGMP; cAMP binding; cGMP binding; ion channel; ion transport; olfaction; transmembr
 F/137-157/Domain: transmembrane #status predicted <TS1>
 F/173-193/Domain: transmembrane #status predicted <TS2>
 F/217-236/Domain: transmembrane #status predicted <TS3>
 F/241-261/Domain: transmembrane #status predicted <TS4>
 F/277-297/Domain: transmembrane #status predicted <TS5>
 F/319-337/Domain: transmembrane #status predicted <TH5>
 F/350-370/Domain: transmembrane #status predicted <TH6>
 F/447-571/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 19.1%; Score 807.5; DB 1; Length 682;
 Best Local Similarity 29.0%; Pred. No. 6.8e-42;
 Matches 192; Conservative 137; Mismatches 256; Indels 77; Gaps 17;

QY 119 PAAPVINEYAD---AQLHNLVKRMQRQRTALYKXKLVGDLSPSPA-----SPQAKPT 168
 Db 55 PSAEMLEAFTQRRPLARLVNLSLEWA--HKSLVETE-QRPDSFLERPRGPOAANDQ 110
 QY 169 AVPPVKESDDKTEHYRLWFKVKQKMLTEYLKRIKLPNSIDSYTDRLYLWLLVTLA 228
 Db 111 SAAPA---DAPKTF-----KERMGEFVVSQSDDIYYWLFIALA 148
 QY 229 --YNNMNCWFIPLRLVFPYQADNIHYNWLIADIIIDYLDMLFIQPLQFVREGDIIIVD 286
 Db 149 SLYNW--IMVARACFDQLODENFVLWGLVDLCVILDTCLRLRTGYLEOGLLVKVD 205
 QY 287 SNELKHYRTSTKPDVAGIIPFDICYFFGN-PMFANRMLKYSFPEFNHLESIMD 346
 Db 206 LAKLDNYIRTLQKLDLFLSLFTLLEFVTVGYPQLRFLRLLRPSRMFEPFQRTETRTN 265
 QY 347 KAYIVRVIRTTGYLLFIHINACVYVWASNYEGIGTTRWVYDGE--VLRCYVWAV 402
 Db 266 YNARFICNLIILYVIIHWNACIYVYAKGLSSDTWVSGQNKTLSCFYVYFVWST 325
 QY 403 RLITIGLPEPQTLFEIVFQLLNFFSGVVFSSLIQMRDVI GAATANQNYFRACMDT 462
 Db 326 LTLTIGEMPPPVKDEYVVFVDFLIGLVIFATIVNIGNSMISNMNAARAEQARDAI 385
 QY 463 IAYNNYSIPKLVQKVRVTEYTWDSQRLMDESLKTLPTTQALAIADVNSISKV 522
 Db 386 KHYMHFRNVSKMEKRVIKFDYLTWNTKTVDKELKYLFDKLRARAIINVHLDLTKV 445
 QY 523 DLFGKCDQMIYDMLRLKSVLYLPQDFVCKKIGKEMVIIKHGEVQVVGDPGDKVLV 582
 Db 446 RIFADCEAGLAVELVQLQPVYSPGYCKKGLIGEMVIIKGLAVV-ADGVTOFV 504
 QY 593 TLKAGSVFGEISLLAAG--GNRRTANVAHGFANLTLTDKTLQELVHYPPSERILM 639
 Db 505 LTAGGCGFGEISILNIGSKAGNRTANIRSIGYSDIFCLSKDLMALTEYDPAKTMLE 564
 QY 640 KKAIVLLKQKAKTAEATP-----PRXDLALLFPKPEETPKLTKLLG---GT 683
 Db 565 BRGEILAKQGLDLSVAAGGLGVIDTEEKVERLDASL-----DILQTRFARLLGETST 619
 QY 684 GKASLARLLKREQA-----AQKENSEGGEEG---KENEDKOKENEDKOKENEDKGE 736
 Db 620 QRLKQRTALERQLCHTGLGLSDNAGEGHAGVPTTHADIHAQPEHTRTSAETNSE 679
 QY 737 NE 738
 Db 680 EE 681

RESULT 11

S11517
 Cyclic nucleotide-activated channel protein - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
 C/Accession: S11517
 R/Phallan, R.S.; Rau, K.W.; Schrader, K.A.; Reed, R.R.
 Nature 347, 184-187, 1990

A;Title: Primary structure and functional expression of a cyclic nucleotide-activated ch
A;Reference number: S11517; MUID:90370115; PMID:1697649
A;Accession: S11517
A;Molecule type: mRNA
A;Residues: 1-664 <DHA>
A;Cross-references: GB:X55519; NID:956791; PIDN:CAA39135.1; PID:956792
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C;Keywords: transmembrane protein
F;456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 19.0%; Score 804; DB 2; Length 664;
Best Local Similarity 29.6%; Pred. No. 1.1e-41;
Matches 219; Conservative 126; Mismatches 286; Indels 108; Gaps 22;
QY 50 ESKLTKSTFTWSEETHNIQDKLKKSSGDLTTPDPQNAABPTGTVPKQ---EMP 106
DB 4 EKSGVKSSPANN---HNHPPPSIKANGKDRAGSRPQSVAAADDTSPFELQAEAMD 60
QY 107 GKEGPNSPQKPAAPVINEYDAQLH-----NLVEMRQRTALYKKLVGDLSSPE 159
DB 61 PRGRGGFQIVRLGVIRDAWANKNFBEPDPDSFLERPR-----GPE 104
QY 160 ASPQAKPTAPVPPVKESDDKPTHEYHLLWFKVKKMPLTEYLKRIKLPSISDYSYDRLYL 219
DB 105 LQVTTTHQGDGKGDEGKGTKKKELEF-----VLDPAGD-WY 143
QY 220 LWLLLVTL--AYNWCWFPLRLVFPYQADNIHYWLIADIICDIILYVDMLEIQLRLOF 277
DB 144 RFLVFIAMPVLYN-CLLV-ARACFDLQRYFVWLVLDYFSDTYIAD-LIIRLRTGF 200
QY 278 VRGDDIVDSNELKHYRTSTKQDLVASIIPEDICYLFFGF-NPMFRANMLKYTSFPE 336
DB 201 LEQGLLVKDKLNDYVHTLQKLDVASIIPDLYFAVGHSPVFRNLLHPARMPE 260
QY 337 FNHLESIMKAYIVIRVTGYLLFILHINACVYASNYEGIGTRWY----DGE-- 390
DB 261 FFDRTERTSPNIFRISNLVYLIVIIHWNACIYVYSKISGFGVDWTYPIITPEYG 320
QY 391 --GNEYLCVYVAVRTLITIGGLPEPOTLPEIFVOLLNPFSGVVFSSLIQMRDVIGAA 448
DB 321 YLAREIYCLYWSLTLLTITGETPPVKDEYLFVIFDFLIGLIVIFATIVGVSGMSLNM 380
QY 449 TANQYFRACMDDTIAYMNNYSIPKLQKRVRTWYVTSQRMDSLLKLTPTTVQL 508
DB 381 NATRAEFQAKIDAVKHWQFRKVSQDEAKVIFDYLTNNKKTIDREVLKMLPAKLA 440
QY 509 ALAIDVNFISIISKVDLPKGDQTMIDYMLLRLKSVLPGDFVCKKGEIGKEMVYIKHGE 568
DB 441 BIATNVHLSLTKVRIIFQDCAGLLVELVLRQVSPGDIICRKGDIKEMVYIKHGE 500
QY 569 VOVLGGPDGKVLVTLKAGSVFGESISLAAG--GNRRTANVVAHGFANLLTLDKKTQL 625
DB 501 LAVV-ADDGVTQYALLSAGSCFGEISILNKGSKWGNRRRTANIRSLGYSDLFCLSKDDL 559
QY 626 EILVHPDSEIRILMKKARVLKQAKTAE---ATPPKDLALLPPKKEETPKLFTLLGG 682
DB 560 EAVTEYDPDAKVLBEERGEILMKGLLDENEVAASMEVDV---QEKLEQLETNM--D 611
QY 683 TGKASLARLLKLRQEAQAKKENSEGGEKENEKQEN--EDKQENEDKGENEDK 740
DB 612 TLYTRFALL-----AYTGAQOKLQRIIVLTIRKQKH---EDDYL 651
QY 741 DKGREPEKPLDRPECTAS 759
DB 652 SDG-----INTPEPTAA 663

RESULT 12

JC6509
rod cyclic nucleotide-gated cation channel protein alpha-chain - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JC6509

R.Veske, A.: Nilsson, S.B.G.; Gal, A.
Gene 202, 115-119, 1997
A;Title: Characterization of canine rod photoreceptor cGMP-gated cation channel alpha-sub
A;Reference number: JC6509; MUID:98087425; PMID:9427553
A;Accession: JC6509
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-691 <VES>
A;Cross-references: EMBL:X9914; NID:9148571; PIDN:CAA68186.1; PID:91488572
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
F;478-602/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 18.9%; Score 801.5; DB 2; Length 691;
Best Local Similarity 29.2%; Pred. No. 1.6e-41;
Matches 220; Conservative 136; Mismatches 286; Indels 112; Gaps 23;
QY 21 QSRNRNEGHPNQSQQTAAQENKEEKSXTKTPTVTSEPHNTIQDKLKKSSSG 80
DB 24 EKEIRRMENGARSS-----FSDDDGDDSDASMEFES---ENETPHA--RUSCNRNSORR 72
QY 81 DLTNPDQNAAPTGTVPKQKEMDPGKGPNSQNPQAPPAAPVINEYADAQLHNLVLRMR 140
DB 73 D-----PSQRE-----QYLPGALALFNWVNSSNKEQEPKKEK 104
QY 141 QRTALYKKLVGDLSSPEASPTAKTAPVPPVKESDDKPTHEYHLLWFKVKKMPLTEY 200
DB 105 KKKK--EKKSXGDKVKNKQDSEKKKKE-----KEKKKXKEK-----GDKK--BEE 150
QY 201 LKRIKLPSISDYSYDRLVLLMLLVTL--AYNWCWFPLRLVFPYQADNIHYWLIADI 258
DB 151 KENVV---IDP-AGNYYNWLFCITLPMVNTW--WVIARACFDLQSDVLEYWIFDY 204
QY 259 ICDDIYLYDMLFIQRLQFVRGDDIIVDSNELKHYRTSTKQDLVASIIPEDICYLFFG 318
DB 205 LSDIVLLDM-FVTRTGTGLEQLLVREBAKLIKYSKNSLOPKLDLSVIPTDLYFLKLG 263
QY 319 FN-PNFRANMLKYTSFPEFNHLSIMDKAVIVIRVTGYLLFILHINACVYASNY 377
DB 264 WYPERLNRLLRISRMEEFFORTETRYNPNIFRISNLVYLIVIIHWNACVYSISKA 323
QY 378 EGIGTRWY----DGE-----GNEYLCVYVAVRTLITIGGLPEPOTLPEIFVOLLNPF 429
DB 324 IGFNDTWVYDVNDPEFGLARKVYSLYWSLTLLTITGETPPVPRDSEYVVFVVDLI 383
QY 430 GYVFVSSLIQMRDVIGAAATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYVTS 489
DB 384 GVLIFATIVGVNIGSMISNNNAARAEQARIDAIKQYMHFRNVSKQMKRVIKWFYLTWN 443
QY 490 QRMLESLLKLTPTTVQLALAIQVNFISIISKVDLPKGDQTMIDYMLLRLKSVLPGD 549
DB 444 KTVDEKEVLKYLPKLRAEIAINVHLDTLKVRIFADCEAGLLVELVLRQVSPG 503
QY 550 FYCKKGEIGKEMVYIKHGEVQVGLGPDGKVLVTLKAGSVFGESISLAAG--GNRRTA 606
DB 504 YICKKGDIKREMYIIEGKLAVV-ADDGITQFVLSGDSYFGEISILNKGSKAGNRRTA 562
QY 607 NVVAHGFANLLTLDKKTQELVHVPDSEIRILMKKARVLKQAKTAE---KTAETAPRKDL 662
DB 563 NIKSISYSLFCLSKDDLMEALTEYPDATKMLBEKKQILMKDGLDINAGSDPKL 622
QY 663 ALLFPKBEETPKLFTLLGGTGKASLARLLKLRQEAQAKKENSEGGEKENEKQKE 722
DB 623 EEKVTREMGSDVLLQI-----RPARIL-----AYESMOOK 653
QY 723 NEDKQKENEKGENEDKD-----KGREPEKPLD 752
DB 654 LKQRLTKVERFLKPIIDTFESALEGTGDSRPLD 687

RESULT 13

S07103
cGMP-gated ion channel protein - bovine
C;Species: Bos primigenius taurus (cattle)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: S07103
 R/Kaupp, U.B.; Nildome, T.; Tanabe, T.; Terada, S.; Boenigk, W.; Stuehmer, W.; Cook, N.J.
 Nature 342, 762-766, 1989
 A>Title: Primary structure and functional expression from complementary DNA of the rod P
 A/Reference number: S07103; MUID:190098076; PMID:2481236
 A/Accession: S07103
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-690 <KAU>
 A/Cross-references: GB:X51604; NID:9203; PIDN:CAA35947.1; PID:9204
 A/Note: part of this sequence was confirmed by protein sequencing
 C/Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
 C/Keywords: cGMP binding; eye; ion channel; ion transport; retina; transmembrane protein
 F:477-601/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 18.8%; Score 797; DB 1; Length 690;
 Best Local Similarity 29.3%; Pred. No. 3,1e-41;
 Matches 212; Conservative 129; Mismatches 282; Indels 100; Gaps 19;

QY 8 VNKVPKIGENNENEGSRNBEQSHPSNQSQTAAQENKGEKSLKTKSPVTSEPHPT 67
 DB 13 VNIPNVGPDVEKEITRMENGACSFSGDDSDASMPFEES-----ETENPHA 59
 QY 68 NIQDKL-SKKNSSGDLTTNPDQNAEPTGVPEKENDPGKGNPSPONKPPAPVINE 126
 DB 60 --RDSFRNTHSGG-----PSQRE-----QYLPFGAIALFNV 89
 QY 127 YADAQLHNLVEMRORTALYKVKLVGDLSSPEASPTAKPTAPVPVKESDKDTEHYR 186
 DB 90 NNSSNKEQEPKEXKXKX--BKSKPDKXNENKXDPKXKXKX---KQDKXKXKX--- 140
 QY 187 LLFWKVKMPLTEYLKRLKPNSSDSYDRLYLWLLVTL--AYNNCWFIPLRLVFPY 244
 DB 141 ----KGDKKEEKEVVDVDPGNTYNN-----WLCITLPVVMYNT--MIARACFDE 189
 QY 245 QTADNIHYWLIADIICDIIVYDMLFIQPLRFQVRGGDIIIVDSNELKHYRTSPKFDLV 304
 DB 190 LQSDVLEWLAFLYDLSVDVYLLDM-FVTRTGYLEQGLVKEERKLDKYSFQKLDV 248
 QY 305 ASIIPFDICYLFFQFN-PMFANRWLYKTSFEPNHHLESIMOKAYIRVIRTTGYLLFI 363
 DB 249 LSVIPTDLXYIKFGWNYPEIRNLRLRISRMFEFFQRTETRTNYPNIFRISNLVWYIII 308
 QY 364 LHINACVYMASNYEGIGTTEWYVDGEGN-----EYLRCYVAVRTLTITIGLPEPQ 415
 DB 309 IHNACVYSISKAIGFNDTWVDPVNDPFGRLARKYVLSLWSTLTITIGETPPV 368
 QY 416 TLFEIVFOLLNFFSGVFFVSSLIQMRDVIQAATANQNYFRACMDDTIAYMNNYSIPKLV 475
 DB 369 RDSYFFVADFLGLVIFATVIGNIGSMISNMAAARAEQARIDAIKQYWHFRNYSKDM 428
 QY 476 QKRYTWTVEYWDQRMDESDILKTLPTTVQALALADVNFISISKVDLPKGDQTMIDY 535
 DB 429 EKRVIKFDYLTWTKTKVDREVLKYLFDKLRABIAINVLHDTLKKVRIADCEAGLLVE 488
 QY 536 MLLRLKSVLYLPGDFVCKKGIGKEMVIIKHGEVQVLGGPDGKVLVTLKAGSVFGEISL 595
 DB 489 LVTLKLPQVYSPGYICKKGDIGREMYIIEKGLAVV-ADGIGTQFVLSDGSYFGEISI 547
 QY 596 LAAGG---GNRTANVAHPANLTLTKTLQBLVHYVDSERILMKKARVLLKKA--- 650
 DB 548 LNIKSGAGNRRTANIKSIGVSDYFCLSKDLMLEALTEYPDAGMLEEKQKILMDGLL 607
 QY 651 --KTAETAPRKDALLPKPEETPKFLTKLLGGTGKASLARLL-----KLKREQAA 700
 DB 608 DINIANGSDPKLEEKVTRMESSVDLLQI-----RRARILAEVSMQKLLKRLTK 659
 QY 701 QKK 703
 DB 660 VEK 662

RESULT 14
 A55251
 Cyclic nucleotide-gated Ca++ channel protein CNG-3 - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 13-Aug-1999
 C/Accession: A55251; S43976
 R/Biel, M.; Zong, X.; Distler, M.; Bosse, E.; Klugbauer, N.; Murakami, M.; Flockerzi, V.;
 Proc. Natl. Acad. Sci. U.S.A. 91, 3505-3509, 1994
 A>Title: Another member of the cyclic nucleotide-gated channel family, expressed in testis
 A/Reference number: A55251; MUID:94224768; PMID:8170936
 A/Accession: A55251
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-706 <BIE>
 A/Cross-references: GB:X76485; NID:9488728; PIDN:CAA54023.1; PID:g488729
 A/Experimental source: kidney
 R/Weyand, I.; Godde, M.; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H.; F
 Nature 368, 859-863, 1994
 A>Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from mam
 A/Reference number: S43976; MUID:94211295; PMID:7512693
 A/Accession: S43976
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-706 <WEY>
 A/Cross-references: GB:X89600; NID:9908823; PIDN:CAA61759.1; PID:g908824
 A/Experimental source: testis
 C/Genetics:
 A/Gene: CNG3
 C/Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
 C/Keywords: cGMP binding; ion channel; ion transport; membrane protein
 F:501-625/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 18.8%; Score 794; DB 2; Length 706;
 Best Local Similarity 29.7%; Pred. No. 4.8e-41;
 Matches 204; Conservative 141; Mismatches 263; Indels 80; Gaps 19;

QY 69 IQDKLSKNSGDLTTNPDQNAEPTGVPEKENDPGKEGP----- 111
 DB 28 IENGSRTHLPCEETSSSELQEGIAEMETRGLEASROSSFTSQGTSLRLIISLRAWSARH 87
 QY 112 -NSPQNKPPAAVINEYADALHNLVEMRORTALYKVKLVGDLSSPE-----ASFPQ 163
 DB 88 LHQEQRPDS--FLERFRGABEQEVSSR-----ESHQFNVGSGQEPDRGRSAMPL 136
 QY 164 TAKPTAVPVKESDDKPTHEHYRLLFWKVKMPLTEYLK--IKLPNSIDSYTRLLYLW 221
 DB 137 ARNNTNTCNNSEKODKAKKE-----KEKBEKENPKKEKKDSYVMDPSNNMYTH 190
 QY 222 L--LLVTLAYNWCNFIPLRLVFPYQTADNIHYWLIADIICDIIVYDMLFIQPLRFQVR 279
 DB 191 LVIAVVPVFNW-CLLV-CRACFDELOSEHLMLWLDYSADILYGMNML-VRARTGELE 247
 QY 280 GDDIIVDSNELKHYRTSTKFLQDVASIIPEICVLPFGFN-PMFANRWLYKTSFPEFN 338
 DB 248 QGLWMDASRLMKWYTOTLHFELDLVSLVPTDLAYFLGMNYPBELRFRNLLKLARLEFF 307
 QY 339 HHLESIMDKAYIRVIRTTGYLLRFLTHNACVYMASNYEGIGTTRWYVDGEGN----- 392
 DB 308 DTETRTNVPMFRICNLVILIIHWNACIYPAISKPIGFGTDSWYFNVNPEVGR 367
 QY 393 --EYLRCYVAVRTLTITIGLPEPQTLFEIVFOLLNFFSGVFFVSSLIQMRDVIQAATA 450
 DB 368 SRKYISLYSWSTLTITIGETPPPKQBEYLFVWIDFLVGLVIFATVIGNVGSMISNNA 427
 QY 451 NONYFRACMDDTIAYMNNYSIPKLVQKVRVTVETWDSQRMLESLLTKTLPTTVQAL 510
 DB 428 SRAEFQAKIDISKQVMPKRVTKDQETVIRWFDYLVANKKTVDEKEVLSLPDKLKA 487
 QY 511 AIDVNFISIISKVDLPKGDQTMIDYDMLRLKSVLYLPGDFVCKKGIGKEMYYIKHGEVQ 570
 DB 488 AINVLHDTLRKVRIFQDCEAGLLVELKLRPAVSPGDIYCKKGDIGREMYIIEKEKLA 547
 QY 571 VLGGPDGTFVLVTLKAGSVFGEISLLAAG---GNRTANVAHPANLTLTKTLQEI 627

Db	548	VV-AEDGITQFVVLGSGSYFGEISILNIKSGKSGNRRTAIRSIGVSDLCFLSKDOLMEA	606
QY	628	LHVHPDSEILMKAR-VLLKQK---AKTAEATPPPKDLALLFPKKEETPKLFTLLGCT	683
Db	607	LTEYPEAKKALEBKQIILKONLIDEEIAKAGADPKDI-----EKKVEHLETSLSL	659
QY	684	GRASLARLL-----KLKREQAQKKN	705
Db	660	-QTRFARLLAEYNATQMKVQRLSQLES	686
RESULT 15			
I50680			
alpha subunit of rod photoreceptor CNG-channel - chicken			
C;Species: Gallus gallus (chicken)			
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999			
C;Accession: I50680			
R;Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.E			
Neuron 10, 865-877, 1993			
A;Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels			
A;Reference number: I50630; MUID:93264082; PMID:7684234			
A;Accession: I50680			
A;Status: preliminary; translated from cB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-645 <BON>			
A;Cross-references: EMBL:X89599; NID:9908852; PIDN:CAA61758.1; PID:9908853			
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>			
F;431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>			
Query Match 18.2%; Score 771; DB 2; Length 645;			
Best Local Similarity 24.3%; Pred. No. 1.1e-39;			
Matches 173; Conservative 104; Mismatches 196; Indels 32; Gaps 12;			
QY	217	LYLLMLLVTL--AYNNWCNFIPLRLVFPYQTDNHIHWLIADIICDIIVLYDMLFIQPR	274
Db	116	MYNNWLFCTIIMPVYNNWT--MILARACFDELQNDYLAWFIVDVYSDVIYIADM-FVTR	172
QY	275	LQFVGGDIIVDSNELKRYTSTKFDLDVASIIPDICYLFGFN-PMERANRMLKYTS	333
Db	173	TGYLEQGLLVKEQKLEKYSLSQFLDFLSIIPTDILLYFKLGLNYPELRINRLRVAR	232
QY	334	FFENHLESIMDKAVTYRVIRTTGYLLFILHINACVYVWASNYEGIGTTRWYDGEFN-	392
Db	233	NPEFFQRTETFTNYPNIFRISNLVMIYIIHWNACVYVWASNYEGIGTTRWYDGEFN-	292
QY	393	-----EYLCRYVAVRTLTITIGLPEPQTLFEIVQLNFFSGVFPVSSLIQOMEDVI	445
Db	293	EFARLTRKYVSLYXWSTLTITIGETPPVPRDSEYFFVVDVFLVGLIFATIVNGVSMI	352
QY	446	GAATANQYFRACDDDTIAYNNYSIPKLQKRVRTWYETWDSQRMLESLLKTLPTT	505
Db	353	SNMNAARAEFOAKIDAIKQYHFRVSKDMKRVIKWFDYLTNKKAVDEREVLKYLDPK	412
QY	506	VQLALADVNFISIISKVDLFGCDTQMIYDMLRLKSVLYLPDGFVCKKEIGKEMVYIK	565
Db	413	LRAEAINVHLETLKKVRAIFADCEAGLVELVLQVQVSPGDIYCRKGDIGREMYIHK	472
QY	566	HGEVQVLGGPQGTAVTLTKAGSVGEISLIAAGS--GNERTANVAHGFANLLTLDKK	622
Db	473	EGLAVV-ADGGVTFQFVVLSDGSGFGEISILNIKSGKSGNRRTAIRSIGVSDLCFLSKD	531
QY	623	TLQELIHYPPDSEILMKAR-VLLKQKAKTAEATPPPKDLALLFPKKEETPKLFTLLG	681
Db	532	DLMEALTEYPPDAKAMLEKQILMKDGLLDIEVANLGS-----PKDLEKV--AYME	583
QY	682	GTG----KASLARLLKLKREQAQK	703
Db	584	GSMRLQTKFARL--LAEYDAQOK	606

Search completed: June 21, 2004, 10:07:51
Job time : 25 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 10:04:22 ; Search time 17 Seconds
(without alignments)
2477.927 Million cell updates/sec

Title: US-09-855-828-1

Perfect score: 4234

Sequence: 1 MFKSLTKYKVKRPIGENNEN.....PSAEGGEVLTIEVKEKAKO 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1949	46.0	909	1	CNG4_HUMAN
2	1920	45.3	1394	1	CNG4_BOVIN
3	850	20.1	694	1	CNG3_HUMAN
4	831.5	19.6	683	1	CNG1_RAT
5	829	19.6	663	1	CNG2_BOVIN
6	823.5	19.4	684	1	CNG1_MOUSE
7	821.5	19.4	735	1	CNG1_CHICK
8	818.5	19.3	664	1	CNG2_RABIT
9	817	19.3	686	1	CNG1_HUMAN
10	807.5	19.1	682	1	CNG1_CTFU
11	804	19.0	664	1	CNG2_RAT
12	801.5	18.9	691	1	CNG1_CANFA
13	797	18.8	690	1	CNG1_BOVIN
14	794	18.8	706	1	CNG3_MOUSE
15	788.5	18.6	733	1	CNG3_MOUSE
16	788.5	18.6	733	1	CNG3_MOUSE
17	777.5	18.4	664	1	CNG3_MOUSE
18	771	18.2	645	1	CNG3_CHICK
19	714	16.9	665	1	CNG3_MOUSE
20	640	15.1	575	1	CNGX_RAT
21	484	11.4	261	1	CNG2_HUMAN
22	427.5	10.1	1175	1	CNG4_MOUSE
23	417.5	9.9	1186	1	CNG4_MOUSE
24	414.5	9.8	1198	1	CNG4_RAT
25	413	9.8	1203	1	CNG4_HUMAN
26	412.5	9.7	910	1	CNG1_MOUSE
27	400.5	9.5	889	1	CNG2_HUMAN
28	400.5	9.5	910	1	CNG1_RAT
29	399	9.4	863	1	CNG2_MOUSE
30	397	9.4	774	1	CNG3_HUMAN
31	396	9.4	834	1	CNG2_RAT
32	389.5	9.2	780	1	CNG3_RAT
33	388.5	9.2	779	1	CNG3_MOUSE

34 385.5 9.1 822 1 HCN1_RABIT
35 382.5 9.0 890 1 HCN1_HUMAN
36 365 8.6 1195 1 KCH7_RAT
37 355 8.4 1195 1 KCH7_MOUSE
38 349 8.2 962 1 KCH1_RAT
39 349 8.2 987 1 KCH1_BOVIN
40 341 8.1 1196 1 KCH7_HUMAN
41 337 8.0 988 1 KCH5_RAT
42 336 7.9 989 1 KCH1_MOUSE
43 335 7.9 988 1 KCH5_HUMAN
44 334 7.9 989 1 KCH1_HUMAN
45 327.5 7.7 1162 1 KCH2_MOUSE

ALIGNMENTS

RESULT 1
CNG4_HUMAN
ID CNG4_HUMAN STANDARD; PRT; 909 AA.
AC Q14028; Q14029;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cyclic-nucleotide-gated cation channel 4 (CNG channel 4) (CNG-4)
DE (CNG4) (Cyclic nucleotide-gated cation channel modulatory subunit).
GN CNGB1 OR CNCG4
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS KCNC2A AND KCNC2B).
RC TISSUE=Retina;
RX MEDLINE=93226050; PubMed=7682292;
RA Chen T.Y., Peng Y.-W., Dhallan R.S., Ahamed B., Reed R.R., Yau K.-W.;
RT "A new subunit of the cyclic nucleotide-gated cation channel in
RT retinal rods.";
RL Nature 362:764-767(1993).
CC -!- SUBUNIT: Heterooligomeric complex with CNGL.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=KCNC2B;
CC IsoId=Q14028-1; Sequence=Displayed;
CC Name=KCNC2A;
CC IsoId=Q14028-2; Sequence=VSP_001110;
CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L15296; AAA65620.1; -;
CC EMBL; L15297; AAA65619.1; -;
CC MIM; 600724; -;
CC GO; GO:0017071; C:intracellular cyclic nucleotide activated cation channel.
CC GO; GO:0005222; F:intracellular cAMP activated cation channel.
CC InterPro; IPR000595; CNMP_binding.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR001622; K+channel_pore.
CC Pfam; PF00027; CNMP_binding; 1.
CC SMART; SM00100; CNMP; 1.
CC PROSITE; PS00888; CNMP_BINDING_1; 1.
CC PROSITE; PS00889; CNMP_BINDING_2; 1.
CC PROSITE; PS50042; CNMP_BINDING_3; 1.

KW Ionic channel; Ion transport; CAMP-binding; Transmembrane;
 KW Multigene family; Alternative splicing;
 FT DOMAIN 1 314 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 315 333 H1 (POTENTIAL).
 FT DOMAIN 334 347 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 348 366 H2 (POTENTIAL).
 FT DOMAIN 367 391 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 392 411 H3 (POTENTIAL).
 FT DOMAIN 412 448 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 449 471 H4 (POTENTIAL).
 FT DOMAIN 472 515 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 516 535 H5 (POTENTIAL).
 FT DOMAIN 536 619 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 620 640 H6 (POTENTIAL).
 FT DOMAIN 641 909 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 9 29 POLY-GLU.
 FT NP_BIND 628 767 CAMP (BY SIMILARITY).
 FT BINDING 688 688 CAMP (POTENTIAL).
 FT BINDING 700 700 CAMP (POTENTIAL).
 FT VARSPLIC 1 286 Missing (in isoform RCNC2A).
 FT SEQUENCE 909 AA; 102285 MW; DC0E754336B6EDDD CRC64;
 Query Match 46.0%; Score 1949; DB 1; Length 909;
 Best Local Similarity 46.2%; Pred. No. 6.6e-105;
 Matches 403; Conservative 122; Mismatches 238; Indels 110; Gaps 18;
 QY 14 IGENNENQSRNREBEGSHPSNQOQTAQB--ENKGE---EKSLLTKSTPTVSEEPHTN 68
 DB 67 VGEBAKAEKAEKAE 126
 QY 69 IQDK-----LSKNSSGDLTTPDPONAAEPTGTVPQEKMDPGKEGN----- 112
 DB 127 VEDTDADSCPLMAENPPS--TVLPSPSPAKSDTLIVPSSASGTHRKLKLPSEDEAEELK 184
 QY 113 --SPONKE-----PAAP-----VINEVADQALNVLKVRKQRTALY 146
 DB 185 ALSPAESPVAWSPTTPKDTGQDRAASTASTNSAIND-----RLQELVLKFKERTEKV 240
 QY 147 KKLVVGDLS----SPEASPTAKTAVPPVKESDDKPT--EHYRLLWFKVKKMPLETEY 200
 DB 241 KEKLIDPDTSDSESPKSPAKAPAPADTKPAEAPVBEHYCDMLCKFKHRPWKY 300
 QY 201 LKRIPLNSIDYDRLYLMLLVTLAYNKNCFIPLRLVFPYOTADNHYMLADIIC 260
 DB 301 ---QFOSIDPLNLMTVLWLFVFWANWNCWLIPIVRWAFPYQTDPNHHMLMDLYC 356
 QY 261 DIIYLDMLFTQPRLOFVRGDIIVDSNELRKHRTSTKFLQDVASIIIPDICYLFFGFN 320
 DB 357 DLIVFLDITVQTRLOFVRGDIITDKKMNNYLYKSRPFMDLLSLPLDLYLKVGVN 416
 QY 321 PMFRANRLKTSPEFNHLESIMDKAYIVRITRTGYLLFILHINACVYVWASVEGI 380
 DB 417 PLLRLPRLCKYMAFEFNSRLESLSKAYYVRITRAYLLYSLHNSCLYVWASAYQGL 476
 QY 381 GTTWVYDGEVNEVLCYVAVRILITIGLPEPOTLFEIVFVOLFNFVGFVFFSSLIQ 440
 DB 477 GSTHWVYDGVNSVIRCYPAVKLITITIGLDPKTLFEIVFOLLNFTGVFAFVWIGQ 536
 QY 441 MRDVIGATANTONFRACMDDTIAYMNYISIPKLVQKRVRTWETVWDSQRMLEDSDLLK 500
 DB 537 MRDVVGAATAGCTYRSQMDSTVYMFYKIPKSVQNRVKTWETVYWHSSQGLDESELMV 596
 QY 501 TLPITVOLALADYNFESIISKVDFKCDTOMIYDMLRLKSLVLYLPDGFVCKKGEIGKE 560
 DB 597 QLPKXRLDLAIDVNYIVSKVALFQSCDRQMIEDMLKRLSVVYLPNDVYCKKGEIGRE 656
 QY 561 MYIIKHGEVQVGGPDGKVLVTLKAGSVFGEISLLAAGGNNRTANVAVHGFANLLTLD 620
 DB 657 MYIIQAGQVQVGGPDGKSVLVTLKAGSVFGEISLLAAGGNNRTANVAVHGFANLLTLD 716
 QY 621 KKTIOELIVHVPDSERILMKARVLLKQAKATBATPPKDLALLPPPKETPKLFTLL 680

717 KKDLNEILVHPESOKLLRKARRMLRSNNK-----PKEKSVLILPPRAGTPKLFNAAL 771
 681 GGTGRAS-----LALLKLKREQAQKENSEGEEGKEKEDKQKEDKQK 728
 772 AMTRGVGGKAGKGLAHLRLKLALEAAKHEEL---VEQAKSQDVKGEGSAAAP 828
 729 ENEDKGE-NEDKXGRPEEKFLDRPECTASPIAV-----EEPHSVRTVLP 776
 829 DQHTPKKATDPAPRTPEPP-OSPPSSPPASLSGCEGEGEPAPPEHSVR----- 882
 777 RGTSRQSLIISMAPSAGGEEVLTIEVKEKAKQ 809
 883 -----ICMSPGPPEGEQILSVKMPEREE 906

RESULT 2
 CNG4_BOVIN STANDARD; PRT; 1394 AA.
 ID CNG4_BOVIN Q28181; Q28082;
 AC Q28181; Q28082;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE 240 kDa protein of rod photoreceptor CNG-channel (Contains: Glutamic acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4 (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel modulatory subunit)).
 DE modulatory subunit).
 GN CNGB1 OR CNGC4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID:9913;
 RN [1]
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96009859; PubMed=7546742;
 RA Koetschen H.G., Illing M., Seifert R., Sesti F., Williams A., Gotzes S., Colville C., Mueller F., Dose A., Godde M., Molday L., Kaupp U.B., Molday R.S.;
 RA "A 240 kDa protein represents the complete beta subunit of the cyclic RT nucleotide-gated channel from rod photoreceptor.";
 RL Neuron 15:627-636 (1995).
 RN [2]
 SEQUENCE OF 454-1394 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=96198098; PubMed=8626431;
 RA Biel M., Zong X., Ludwig A., Sautter A., Hofmann F.;
 RA "Molecular cloning and expression of the modulatory subunit of the cyclic nucleotide-gated cation channel.";
 RL J. Biol. Chem. 271:6349-6355 (1996).
 RN [3]
 SEQUENCE OF 1-590 FROM N.A.
 RC TISSUE=Retina;
 RX Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
 RL Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBUNIT: Forms functional heterooligomeric channels with CNG3.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=alternative splicing; Named isoforms=3;
 CC Comment=isoform CNG4D is the most frequent isoform (CNG4D:CNG4C:CNG4E = 20:2:1) in testis;
 CC Name=CNG4C;
 CC ISOID=Q28181-1; Sequence=Displayed;
 CC Name=CNG4D;
 CC ISOID=Q28181-2; Sequence=VSP_001109;
 CC Name=CNG4E;
 CC ISOID=Q28181-3; Sequence=VSP_001108;
 CC -!- TISSUE SPECIFICITY: Retina, testis, kidney, heart and brain.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

DR	InterPro; IPR005821; Ion trans.	
DR	InterPro; IPR001622; K+channel_pore.	
DR	Pfam; PF00027; CNMP binding; 1.	
DR	Pfam; PF00520; ion trans; 1.	
DR	SMART; SM00100; CNMP; 1.	
DR	PROSITE; PS00888; CNMP BINDING 1; 1.	
DR	PROSITE; PS00889; CNMP BINDING 2; 1.	
DR	PROSITE; PS00892; CNMP BINDING 3; 1.	
KW	Ion channel; ion transport; CAMP-binding; Transmembrane;	
KW	Multigene family; Olfaction.	
FT	DOMAIN 1 140	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 141 160	H1 (POTENTIAL).
FT	DOMAIN 161 173	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 174 192	H2 (POTENTIAL).
FT	DOMAIN 193 216	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 217 236	H3 (POTENTIAL).
FT	DOMAIN 237 274	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 275 297	H4 (POTENTIAL).
FT	DOMAIN 298 349	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 350 369	H5 (POTENTIAL).
FT	DOMAIN 370 453	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 454 474	H6 (POTENTIAL).
FT	DOMAIN 475 664	CYTOPLASMIC (POTENTIAL).
FT	NP BIND 462 584	CAMP (BY SIMILARITY).
FT	BINDING 521 521	CAMP (POTENTIAL).
FT	BINDING 536 536	CAMP (POTENTIAL).
FT	CARBOHYD 379 379	N-LINKED (GLCNAC...) (POTENTIAL).
SQ	SEQUENCE 664 AA; 76205 MW; 5E9170D0B322B3E9 CRC64;	
Query Match		
Best Local Similarity 29.7%; Pred. No. 6.1e-40;		
Matches 218; Conservative 127; Mismatches 289; Indels 99; Gaps 20;		
QY	50 EKSILKTKSTVTSEEPHTNIQDKLSKNSSGDLTNPDPONAAEPGTVPQK--EMDPG 107	
Db	3 EKNGVKSSPANN---HNNVPTATIKANGKDESTRSRQSAADDDTSSELQRLAEMDAP 59	
QY	108 KEGNSPQNKPPAAPVINEVA-----DAQLNLRMRQRTALYKKLVGEGDLSSPA 160	
Db	60 QQRGGFRIRVLVGVIRQWNRNFRFEARPDPSFLERF-----GPEL 103	
QY	161 SPQTAKTAVPPVKESDDKTEHYRLLWFKVKKMPLTEYLKILPNSIDSYTDRLYLL 220	
Db	104 QTVTQGGDKGDKGDKGDKKKKFLF-----VLDPAQD-WYR 142	
QY	221 WLLIVLT--AYNNCWFPIRLVFPYQADNIHLYLIADIICDIYLYDMLFTQPKLQFV 278	
Db	143 WLFVIAMPVLYNW-CLLV-ARACFSDLRQGVFLWLVLDVFDVWYIAD-LFIRLRTGFL 199	
QY	279 RGGDIIVDSNELRKHHTSTKFLQDVASIIIPFCICYLFFGF-NMPFRANRMLKXTSFFEF 337	
Db	200 EQGLLVKDPKLRDNYIHTLQFKLDVASIITPTDLIFAVGIHNPURFNLLHFAFMPEF 259	
QY	338 NHLESIMDKAYIVRVITRTGYLLFILHINACVYVWASNYEGIGTTWVY----DGE-- 390	
Db	260 FDRTEITSYFNIRISNLVLYLVIHWNACIYAIKSGIGFQVDVWVYFNITDPEYGY 319	
QY	391 -GNEYLCYVAVKTLTITIGLPEPQTLFEIVPOLNFFSGVFVSSLIQMDRVDIGAAAT 449	
Db	320 LAREYIYCLVWSTLTATIGETPPPVKDBEYLFVIFDPLIGVLIATVNGVSGMSINNM 379	
QY	450 ANQNVFRACDDTAYMNNYSIPKLQKRVETVYETWDSORMLDESLDKTLPTTVQLA 509	
Db	380 ATRAEFAQIDAVGHYHQFRKVSKEAKVWKWFEDYLWTKVTVDREVLKQLPAKLRAE 439	
QY	510 LAIDVNFYSIIISKVFLFKGCDTQMTYDMLLRKSLVLYLPQDFVCKKGIGKEMIIKGEV 569	
Db	440 IAINVHLSTLKKVIRFQDCEAGLLVELVLKRPQVFGFDYICRKGIGKEMIIKGEKL 499	
QY	570 QVLGPDGTQVLVTLKAGSVGEISLLAAG--GNERTANVVAHGFANLLTDKKTQLE 626	
Db	500 AVV-ADGGVTQYALLSAGCFEISILNKGSKVGNRTANIRSLGIGSDLFCLSKDDLME 558	
QY	627 ILVHPDSEIRILMKARVLKQAKTAE---ATPPRKDALALLPPPKETPKLFTLLGGT 683	
Db	559 AVTEYPPDAKKVLEERGRIILMKSGLLDENEVAASMEVDVQEKLKQLETNNTLYTRPG-- 616	
QY	684 GKASLARILLKLKREQAQKENSEGGEKEKEDKCKEN--EDKOKENEDKCKENEDKD 741	
Db	617 -----RL-----AYTGAQQLKORITVLEVKQKQNT-----DDYLS 651	
QY	742 KGREPEEKPLDRP 754	
Db	652 GMNSPEFAAAEQP 664	
RESULT 9		
CNGL HUMAN STANDARD; PRT: 686 AA.		
ID	CNGL HUMAN	STANDARD; PRT: 686 AA.
AC	P29973; Q16279; Q16485;	
DT	01-APR-1993 (Rel. 25, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	15-MAR-2004 (Rel. 43, Last annotation update)	
DE	CGMP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNGL)	
DE	(Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated	
DE	channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)	
DE	(Rod photoreceptor cGMP-gated channel alpha subunit).	
GN	CNGL OR CNCGI OR CNCG.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1] SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Retina;	
RX	MEDLINE=92210603; PubMed=1372902;	
RA	Pittler S.J., Lee A.K., Altherer M.R., Howard T.A., Seldin M.F.,	
RA	Hurwitz R.L., Wasmuth J.J., Baehr W.;	
RT	"Primary structure and chromosomal localization of human and mouse	
RT	rod photoreceptor cGMP-gated cation channel.";	
RL	J. Biol. Chem. 267:6257-6262(1992).	
RN	[2] SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Retina;	
RX	MEDLINE=92356211; PubMed=1379636;	
RA	Dhallan R.S., Macke J.P., Bddy R.L., Shows T.B., Reed R.R.,	
RA	Yau K.-W., Nathans J.;	
RT	"Human rod photoreceptor cGMP-gated channel; amino acid sequence,	
RT	gene structure, and functional expression.";	
RL	J. Neurosci. 12:3248-3256(1992).	
RN	[3] SEQUENCE OF 313-573 FROM N.A.	
RP	SEQUENCE OF 313-573 FROM N.A.	
RX	MEDLINE=95175019; PubMed=7532814;	
RA	Discler M., Biel M., Flockezi V., Hofmann F.;	
RT	"Expression of cyclic nucleotide-gated cation channels in non-sensory	
RT	tissues and cells.";	
RL	Neuropharmacology 33:1275-1282(1994).	
RN	[4] VARIANT ARRP PHE-316, AND VARIANTS GLN-28 AND ASN-114.	
RP	VARIANT ARRP PHE-316, AND VARIANTS GLN-28 AND ASN-114.	
RX	MEDLINE=96036047; PubMed=7479749;	
RA	Driva T.P., Finn J.T., Peng Y.-W., McGee T.L., Berson E.L., Yau K.-W.;	
RT	"Mutations in the gene encoding the alpha subunit of the rod	
RT	cGMP-gated channel in autosomal recessive retinitis pigmentosa.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 92:10177-10181(1995).	
CC	-1- FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN	
CC	COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN	
CC	BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO AN OPENING OF THE CATION	
CC	CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD	
CC	PHOTORECEPTORS.	
CC	-1- SUBUNIT: Homotetramer or higher oligomer. Forms heterooligomeric	
CC	complex with CNGL.	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	-1- TISSUE SPECIFICITY: Rod cells in the retina.	
CC	-1- DISEASE: Defects in CNGL are a cause of autosomal recessive	
CC	retinitis pigmentosa (ARRP) [MIM:123825]. ARRP is a disease that	
CC	leads to degeneration of retinal photoreceptor cells.	

CC CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -!- DATABASE: NAME=Mutations of the CNGB1 gene;
 CC NOTE=Retina International's Scientific Newsletter;
 CC WWW="http://www.retina-international.com/sci-news/cngalmut.htm".
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC
 CC EMBL; M84741; AAA52010.1; ALT_INIT.
 CC EMBL; S42457; AAB22778.1;
 CC EMBL; S76062; AAB14206.1;
 CC FIR; A42161; A42161.
 CC Genew; HGNC:2148; CNGB1.
 CC MIM; 123825; -.
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0006810; P:transport; TAS.
 CC GO; GO:0007601; P:vision; TAS.
 CC InterPro; IPR000595; CNMP_binding.
 CC InterPro; IPR005821; ion_trans.
 CC InterPro; IPR001622; K+channel_pore.
 CC Pfam; PF00027; CNMP_binding; 1.
 CC Pfam; PF00520; ion_trans; 1.
 CC SMART; SM00100; CNMP; 1.
 CC PROSITE; PS00888; CNMP_BINDING_1; 1.
 CC PROSITE; PS00889; CNMP_BINDING_2; 1.
 CC PROSITE; PS0042; CNMP_BINDING_3; 1.
 CC Ionic channel; ion transport; CGMP-binding; Transmembrane;
 CC Multigene family; Vision; Disease mutation; Polymorphism;
 CC Retinitis pigmentosa.
 CC KW DOMAIN 1 160 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 151 181 H1 (POTENTIAL).
 CC FT DOMAIN 182 194 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 195 213 H2 (POTENTIAL).
 CC FT DOMAIN 214 237 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 238 257 H3 (POTENTIAL).
 CC FT DOMAIN 258 295 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 296 318 H4 (POTENTIAL).
 CC FT DOMAIN 319 370 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 371 390 H5 (POTENTIAL).
 CC FT DOMAIN 391 474 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 475 495 H6 (POTENTIAL).
 CC FT DOMAIN 496 686 CYTOPLASMIC (POTENTIAL).
 CC FT NP_BIND 687 605 CGMP (POTENTIAL).
 CC FT BINDING 542 542 CGMP (POTENTIAL).
 CC FT BINDING 557 557 CGMP (POTENTIAL).
 CC FT CARBOHYD 421 421 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT VARIANT 28 28 R -> Q.
 CC FT VARIANT 114 114 /FTID=VAR_009295.
 CC FT VARIANT 316 316 D -> N.
 CC FT VARIANT 316 316 S -> F (in ARR).
 CC FT VARIANT 316 316 /FTID=VAR_009297.
 CC FT CONFLICT 46 46 S -> Y (IN REF. 1).
 CC FT CONFLICT 85 85 L -> I (IN REF. 1).
 CC FT CONFLICT 146 147 EE -> HH (IN REF. 1).
 CC FT CONFLICT 539 539 Y -> T (IN REF. 1).
 CC FT CONFLICT 677 678 GA -> WS (IN REF. 1).
 CC FT SEQUENCE 686 AA; 79126 MW; E5200D216FC97AF6 CRC64;
 CC
 CC Query Match 19.3%; Score 817; DB 1; Length 686;
 CC Best Local Similarity 29.9%; Pred. No. 7.7e-40;
 CC Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;
 CC
 CC 5 LTKVNVKPTIGENNEQSSRRNEEGSHPS---NQSQQTAAQENKGE---KSL 53
 CC 13 VTMPNVIVP-----DIEKEIRRMENGACSFSEDDSDASTSESENENPHARGSFYSKL 67

QY 54 KTKSTPTVSEBHTNIQDKLSKKNSSGDLTTPDPONAAAPTGTVPPEQKEMPQKGGPNS 113
 DB 68 R-KGFSQREQVLPGAIALFNVNSS-----NKD-----QEPBEKKKKKKKKSKDDKNE 117
 QY 114 PQNKPPAAPVINEYADAQLHLVTKMRORTALYKKLVKGLVEGDISSPEASQTKAPTAVPV 173
 DB 118 NKNDPE-----KKKKKKKKKK-----E 137
 QY 174 KESDDKPTHYVLLMFKVKKMPLTEYLKRIKLPNSIDSYDRLYLLMLLVL--AYNW 231
 DB 138 EKSKDKKEE-----KKEVV-----IDP-SGTYNNMLFCITLPMVNW 176
 QY 232 NCWFILRLVFPVQVADNTHYLLADIICDIIYLDMLFIQPLQFVGGDIIVDSNEIR 291
 DB 177 T--MVIARACFDELOSDYLEYLLILOYSDIVYLIDM-FVTRTGYLBSGLLVKEELKLI 233
 QY 292 KHYRTSKFQLDVASIIPEDICYLFFGFN-PMFRANRMLKYSFFEFNHLESIMDKAYI 350
 DB 234 NKYSNQLQKLDVLSLIPDILLYFKLGMWYPEIRLNRLLRPSRMEFFQRTETRTNYENI 293
 QY 351 YVIRTGTGYYLLHILHINACVYTWASNYEGIGTRVY-----DGE-----GNEYLRICYWAV 402
 DB 294 FRISNLVMTYIIIIHWNACVYSISKAGFGNDTWYDPINDPEFRGLARKYVYSLYWST 353
 QY 403 RTLITIGLPEPQTLFEIVFQLLNFPFSGVFPSSLIGQMRDVGAATANQVYFRACMDT 462
 DB 354 LTLITIGETPPVRDSEYVFWVDLIGVLIFATIVGNIGSWISNNAARAEFQARIDAI 413
 QY 463 IAYMNYISIPKLVQKRVRTWBYTWDSQRMDELSDLLKTLPTTVOLALADNFSIISKV 522
 DB 414 KQMEFRNVSKDMKRVKWFEDYLTWNTKTVDEKVLKYPDKLRAETAINVHLDLTKV 473
 QY 523 DLFGKGDQMIYDMLRLKSLVLYLPGDVKCKGEGEKEMWIIKHGEVOLGPGDGTQV 582
 DB 474 RIFADCEAGLLVELVLKLOPVYSPDYICKGDIGRMYIIKGGKLAIV-ADGVTFV 532
 QY 583 TLKAGSVFGEISLLAAG---GNRTANVVAHGFANLLTLDKTLQELVHYVPSERILM 639
 DB 533 VLSGSGVFEISILNIKSGKAGNRRTANIKSIGSDLPCLSKDDLMALTEYDPAKTMLE 592
 QY 640 KKAIVLLKKA-----KTAETPPKDLALLPPKKEE-PKPKTLGGTGKASLARLL--- 692
 DB 593 EKGQILMKDGLLDLNTIANAGSDPKLEEKVTREMGSVDLLOQT-----RPARILAEY 644
 QY 693 -----KLKREQAOKK-----ENSEG-GEEG 713
 DB 645 ESMQKQKRLTKVEKFLKPLIDTEFFSIEGPGAESG 681
 RESULT 10
 CNG ICTPU
 ID CNG ICTPU STANDARD; PRT; 682 AA.
 AC P55934;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic-nucleotide-gated cation channel.
 OS Ictalarus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory neuroepithelium;
 RX MEDLINE=92110008; PubMed=1370374;
 RA Goulding E.H., Ngai J., Kramer R.H., Colicos S., Axel R.,
 RA Siegelbaum S.A., Chess A.,
 RT "Molecular cloning and single-channel properties of the cyclic
 RT nucleotide-gated channel from catfish olfactory neurons.";
 RL Neuron 8:45-58(1992).
 CC -!- FUNCTION: This cyclic nucleotide-gated channel is activated

equally well by both cAMP and cGMP.
 CC -!- TISSUE SPECIFICITY: Olfactory neurons.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M83111; -, NOT_ANNOTATED_CDS.
 CC PIR; JH0560; JH0560.
 CC InterPro; IPR000595; cNMP binding.
 CC InterPro; IPR005821; Ion trans.
 CC InterPro; IPR001622; K+channel pore.
 CC InterPro; IPR001201; PAP_25A_core.
 CC Pfam; PF00027; cNMP_binding; 1.
 CC Pfam; PF00520; Ion_trans; 1.
 CC SMART; SM00100; cNMP; 1.
 CC PROSITE; PS00888; cNMP_BINDING_1; 1.
 CC PROSITE; PS00889; cNMP_BINDING_2; 1.
 CC PROSITE; PS00890; cNMP_BINDING_3; 1.
 CC Olfaction; Ion transport; Ionic channel; cAMP-binding; cGMP-binding;
 CC Transmembrane. 1
 CC DOMAIN 136 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 137 H1 (POTENTIAL).
 CC DOMAIN 157 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 158 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 170 H2 (POTENTIAL).
 CC TRANSMEM 171 H2 (POTENTIAL).
 CC DOMAIN 191 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 192 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 219 H3 (POTENTIAL).
 CC TRANSMEM 220 H3 (POTENTIAL).
 CC DOMAIN 240 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 241 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 273 H4 (POTENTIAL).
 CC TRANSMEM 274 H4 (POTENTIAL).
 CC DOMAIN 311 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 312 H5 (POTENTIAL).
 CC DOMAIN 332 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 333 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 344 H6 (POTENTIAL).
 CC TRANSMEM 345 H6 (POTENTIAL).
 CC DOMAIN 365 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 366 CYTOPLASMIC (POTENTIAL).
 CC NP_BIND 455 CAMP (BY SIMILARITY).
 CC BINDING 514 CAMP (POTENTIAL).
 CC BINDING 514 CAMP (POTENTIAL).
 CC BINDING 529 CAMP (POTENTIAL).
 CC SEQUENCE 682 AA; 78020 MW; 2C78597DC2C74F75 CRC64;
 Query Match 19.1%; Score 807.5; DB 1; Length 682;
 Best Local Similarity 29.0%; Pred. No. 2.7e-39;
 Matches 192; Conservative 137; Mismatches 256; Indels 77; Gaps 17;
 QY 119 PAAPVINEYAD- AQLNIVKMRQRTALYKKVGLDLSPEA-----SPQAKPT 168
 Db 55 PSAEMLEAFTQRRPLARLVNLVLSREWA---HKSLVETE-QRPDSFLFRPGPQAANDQ 110
 QY 169 AVPPVKESDDKPTHEYHYLLWFKVKQKPLTEYLKRIKLPNSIDSYTRDLVLLVLLVTLA 228
 Db 111 SAAPA-----DAPKTF-----KEREGFVVSQSDIYYWVFFIALA 148
 QY 229 -YNNWNCIFPLRLVFPYQADNHYWLIADIICDIYLYDMLFIQPRQLQVRCGDIIVD 286
 Db 149 SLYNW--IMLVARACFDQQLDENPFLWGLVLCVIVILDTCLRLRTGYLEQGLVAKD 205
 QY 287 SNELKHYRTSTKFDVASIIPDCIVLFGFPMFPAERMLKYTSFEFENHLESIMD 346
 Db 206 LAKLRDNYRTLOKFLDLSILTELLFFVTVGYVQPLFNRLFRSMFEFDDTERTN 265
 QY 347 KAYIVRVIRTTGILLFILHINACVYMASNVEGIGTTRWVYDGEENE-----YLRCYWAV 402
 Db 266 YPNAFCINLIYILVIHWNACIYVYALSKALGLSDTWVYSGQNTLSFCYVCYFWST 325
 QY 403 RFLITIGLPEPQTLFEIVFQQLNFFSGVFFSSILGQVRDVIQAATANYFACWDDT 462
 Db 326 LTLTITIGEMPPPVKDEEYVYVDFLVGLVIFATIVGVNGSMIANNATRAEFQTRIDAI 385

QY 463 IAYMNNYSIPKLVQKRVRTWYETWDSQRMDESDLLKTLPTTVQLALAIQVNFYSISKV 522
 Db 386 KHYMHFKVNTLETRVTKWFDYLTWNTKVTDEQVLEKLPDKLRAEIALNVHLDLTKKV 445
 QY 523 DLFKGGDTOMIYMLKLSVLYLPDGFVCKKGEIKGEMVYIKHGEVQVNLGGPDGTVLV 582
 Db 446 RIFQDCEAGLLVELVLRPQWSPGYICRKGDIKEMVYIKHGEVQVNLGGPDGTVLV 504
 QY 593 TLKAGSVFGEISLLAAGG---GNRRTANVVAHGPNALLTLDKKTLOEILVHYPSERILM 639
 Db 505 LLTLAGGCGEISILNIQSKMGKRNRTANIRSIGVSDFLCFLSKDLMKVAEYPAQKVL 564
 QY 640 KKARVLLKQAKTAAATP-----PRKDLALLPPPKETPKLFTILG---GT 683
 Db 565 ERGREILRKQGLLDESVAAGGLGVIDTEEKVERLDASL-----DILQTRFARDLGEFTST 619
 QY 684 GKASLARLLKLRBOA-----AQKENSEGGEGE---KENEDKQKNEKQKNEKQK 736
 Db 620 QRRLKQRTALEROCHTGLGLLSDNEAGEHAGVPTHADIHAQETHRTSAETNSE 679
 QY 737 NE 738
 Db 680 EE 681
 RESULT 11
 CNG2 RAT STANDARD; PRT; 664 AA.
 ID CNG2 RAT Q00195;
 AC Q00195;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleotide-gated
 DE cation channel 2) (CNG channel 2) (CNG2) (CNC1).
 GN CNG2 OR CNG2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory sensory neuron;
 RX MEDLINE=90370115; PubMed=1697649;
 RA Dhallan R.S., Yau K.-W., Schrader K.A., Reed R.R.;
 RT "Primary structure and functional expression of a cyclic nucleotide-
 RT activated channel from olfactory neurons.";
 RL Nature 347:184-187(1990).
 CC -!- FUNCTION: Odorant signal transduction is probably mediated by a G-
 CC protein coupled cascade using cAMP as second messenger. The
 CC olfactory channel can be shown to be activated by cyclic
 CC nucleotides which leads to a depolarization of olfactory sensory
 CC neurons.
 CC -!- SUBUNIT: Heterooligomer of CNCL1 and CNCL2 subunits.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Olfactory neurons.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -!- CAUTION: It is uncertain whether Met-1 or Met-2 is the initiator.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X55519; CAA39135.1; -.
 CC PIR; S11517; S11517.
 CC InterPro; IPR000595; cNMP binding.
 CC InterPro; IPR005821; Ion_Trans.

DR	InterPro: IPR001622; K+channel_pore.	QY	626	EILVHPDPSERILMKARVLLKOKAKTAE---ATPRKDLALFPKERTPKLFTLLGG	682
DR	Pfam: PF00027; CNMP binding; 1.	Db	560	EAVTEYPAKVLLEGRILMKLEGLLDENVAASMEVDV---QEKLEQLTNN--D	611
DR	SMART: SM0100; CNMP; 1.	QY	683	TGRASLARLLKREQAQKENSEGEGEKEDKOKEN--EDQKQENEDKGENEDK	740
DR	PROSITE; PS00888; CNMP_BINDING_1; 1.	Db	612	TLTYRFAILL-----AETGAQKKQKQRTIVLETKQKNH-----EDDYL	651
DR	PROSITE; PS00889; CNMP_BINDING_2; 1.	QY	741	DKGRPEPEKPLDRPECTAS	759
DR	PROSITE; PS0042; CNMP_BINDING_3; 1.	Db	652	SDG-----INTPEPTAA	663
KW	Ionic channel; Ion transport; CAMP-binding; Transmembrane;				
KW	Multigene family; Olfaction.				
FT	DOMAIN 1 142				
FT	TRANSMEM 143				
FT	DOMAIN 163				
FT	TRANSMEM 176				
FT	DOMAIN 195				
FT	TRANSMEM 219				
FT	DOMAIN 238				
FT	TRANSMEM 277				
FT	DOMAIN 300				
FT	TRANSMEM 352				
FT	DOMAIN 372				
FT	TRANSMEM 456				
FT	DOMAIN 477				
FT	NP BIND 464				
FT	BINDING 523				
FT	BINDING 538				
FT	CARBOHYD 381				
FT	VARIANT 212				
SQ	SEQUENCE 664 AA; 76176 MW; 720806950EC27F3C CRC64;				
Query Match					
Best Local Similarity 19.0%; Score 804; DB 1; Length 664;					
Matches 219; Conservative 126; Mismatches 286; Indels 108; Gaps 22;					
QY	50	EKSLKTKTPVTSEPHNTIQQDKLSKNSGDLTTPDPQNAEPTGTVPQEK---	BMDP	106	
Db	4	EKSNVGVKSSPANN---HNHPPPSIKANGKDDHAGSRPQSVAAADDTSPQLAEMDT	60		
QY	107	GKEGNSQNPQAPVINEVADQLH-----NLVKRMQRTALYKKLVEGDJSSPE	159		
Db	61	PRRGGRGQRIURLVGVIRWDANKFNFRPEEPDPSFLERFR-----GPE	104		
QY	160	ASPTAKPTAVPPVKESDDKTEHYKLLWFKVKKMPLTEYLKILKLPNSIDSYDRLYL	219		
Db	105	LQTVTHQDDKGGKGGKTKKKKFLF-----VLDPAGD-WYY	143		
QY	220	LWLLLVTL--AYNNCWPIPLRVFPYQTDNIHWLIADIICDIYLYDMLFIQRLQF	277		
Db	144	RWLFVIAMPVLVNW-CLLV-ARACFSQLQRYFVWVLVDVFSVTYVIAD-LIIRLTGF	200		
QY	278	VRGDIIVDSNELKHYRTSKFOLDVASIIPDICVLFPGF-NPMFRANMLKYTSFFE	336		
Db	201	LEQGLLVKDPKKRDNIHTIQKLDVASIIPDIIYFVAGIHSPEVFRNLLHFARME	260		
QY	337	FNHLESIMDKAYIRVIRITGYLLFLILHINACVYVWASNYEGITGRWVY-----DGE--	390		
Db	261	FFDRTERTSYPNIFRISNLVLYLIIHWNACIYVVISKISGFGVDVWYVNPITDPEYG	320		
QY	391	--GNEYLRCVYVARTLITIGLPEPQTLPEIYVOLLNFFSGVFFVSSLLGQMRDVIGA	448		
Db	321	YLAREYICLYWSLTLTITIGETPPVPKDBEYLFVDFLFIATVGVNVSIMN	380		
QY	449	TANQNYFRACDDTIATMNNYSIPKLQKVRVWYETWDSQRMLESLLKTLPTVOL	508		
Db	381	NATRAEFOAKIDAVKHYWQFRKYSKOMEAKVKKFVLYWTKNTVDERVILKLPKLA	440		
QY	509	ALADYNFSIISKVDLFKGCDDQIMVDMRLKSLVLPFGDFVCKGEGTKENYIIKHGE	568		
Db	441	EIAINHLSTLKKVIRFQDCAGLLVELVLRQVPSQDYICRKGDIKGMYYIIKEGK	500		
QY	569	VOVLGGPDGTVLVLTKAGSVFGEISLLAAGG---GNRRATANVVAHFANLLTLDKTLQ	625		
Db	501	LAVV-ADDGVTQVALLSAGSCFGEISILNFKSGMGNRRATNIRSLGYSDLCFLSKDDLM	559		

RESULT 12

CNG1_CANFA STANDARD; PRT; 691 AA.

AC Q28279; DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE CNGP-gated cation channel alpha 1 (CNG channel alpha 1) (CNG-1) (CNG1)

DE (Cyclic nucleotide-gated channel alpha 1) (Cyclic nucleotide-gated channel, photoreceptor) (Cyclic-nucleotide-gated cation channel 1)

DE (Rod photoreceptor cGMP-gated channel alpha subunit).

GN CNG1 OR CNGC.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Beagle X Briard;

RA Veske A.;

RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97415722; PubMed=9268598;

RA Zhang Q., Pearce-Kelling S., Acland G.M., Aguirre G.D., Ray K.;

RT "Canine rod photoreceptor cGMP-gated channel protein alpha-subunit: studies on the expression of the gene and characterization of the cDNA."

RT Exp. Eye Res. 65:301-309(1997).

CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein coupled cascade using cGMP as second messenger. This protein can be activated by cGMP which leads to an opening of the cation channel and thereby causing a depolarization of rod photoreceptors.

CC -!- SUBUNIT: Homotrimer or higher oligomer.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel (TC 1.A.1.5) family.

CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch).

CC EMBL: X9914; CA68186.1; -

CC EMBL: U83905; AB61707.1; -

CC FIRM: J06509; J06509.

CC InterPro: IPR00595; CNMP binding.

CC InterPro: IPR005821; Ion trans.

CC InterPro: IPR001622; K-channel_pore.

CC Pfam: PF00027; CNMP binding; 1.

CC Pfam: PF00520; Ion trans; 1.

CC SMART: SM00100; CNMP; 1.

CC PROSITE; PS00888; CNMP_BINDING_1; 1.

CC PROSITE; PS00889; CNMP_BINDING_2; 1.

CC PROSITE; PS0042; CNMP_BINDING_3; 1.

CC EMBL; X51604; CAA35947.1; -
 DR PIR; S07103; S07103.
 DR InterPro; IPR00595; CNMP_binding.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K+channel_pore.
 DR Pfam; PF00027; CNMP_binding; 1.
 DR Pfam; PF00520; Ion_trans; 1.
 DR SMART; SM00100; CNMP; 1.
 DR PROSITE; PS00888; CNMP_BINDING_1; 1.
 DR PROSITE; PS00889; CNMP_BINDING_2; 1.
 DR PROSITE; PS00442; CNMP_BINDING_3; 1.
 KW Ionic channel; Ion transport; CGMP-binding; Transmembrane;
 Multigene family; Vision.
 FT DOMAIN 1 162
 FT TRANSMEM 163 183
 FT H1 (PROBABLE).
 FT DOMAIN 184 196
 FT EXTRACELLULAR (PROBABLE).
 FT DOMAIN 197 215
 FT H2 (PROBABLE).
 FT DOMAIN 216 239
 FT CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 240 259
 FT H3 (PROBABLE).
 FT DOMAIN 260 297
 FT EXTRACELLULAR (PROBABLE).
 FT TRANSMEM 298 320
 FT H4 (PROBABLE).
 FT DOMAIN 321 372
 FT CYTOPLASMIC (PROBABLE).
 FT TRANSMEM 373 392
 FT H5 (PROBABLE).
 FT DOMAIN 393 476
 FT EXTRACELLULAR (PROBABLE).
 FT TRANSMEM 477 497
 FT H6 (PROBABLE).
 FT DOMAIN 498 690
 FT CYTOPLASMIC (PROBABLE).
 FT NP_BIND 485 607
 FT BINDING 544 544
 FT CGMP (POTENTIAL).
 FT BINDING 559 559
 FT CGMP (POTENTIAL).
 FT CARBOHYD 423 423
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 690 AA; 79602 MW; A0LCF6567424455 CRC64;
 Query Match 18.8%; Score 797; DB 1; Length 690;
 Best Local Similarity 29.3%; Pred. No. 1.1e-38;
 Matches 212; Conservative 129; Mismatches 282; Indels 100; Gaps 19;
 QY 8 VNKVPIGNNENEGSSRRNEGHPNSQSOQTAAQENKGEKSLTKTPVTSERPHT 67
 DB 13 VNIPNVGPDVEKETRMENAGCSFSGDDDDDSAMFEES-----ETENPHA 59
 QY 68 NIQDL-SKQSSGDLITNPQNAAEPTGTVPQKEMDPGKGNPQKPPAAYINE 126
 DB 60 --RDSFRSNTGSGQ-----PSQRE-----QYLPGAIALFNV 89
 QY 127 YADAQLHNLVGRMORTALYKXKLVEGLSPSPASQTAKTAVPPVKESDDKTEHYR 186
 DB 90 NNSNKEQEPKPKKKKK--BKSGKPDKNENKDKPKKKKE---KDKDKKKES--- 140
 QY 187 LLWFVKVKMPLTEYLKRIKLPNSIDSVTRDYLWLLLVTL--AYNWNCFPIPLRLVFPY 244
 DB 141 ----KGDKKKEKKEVVVDPSGNTYNN----WLCITLPVWYNT--NIIARACFDE 189
 QY 245 QTANIHWLADIICIIYLYMLFQIPROFVRGGDIIVDSNELKHYRTSTKFDVY 304
 DB 190 LQSDYLEWLAFLDVLSDVYLLDN-FVTRTRGYLEQGLLVKEERLIDKYKSTFQFKLDV 248
 QY 305 ASIIPEDICYLFFGN-PMFRANRLKLYTSFENHLESIMDKAYIYRVRTTGYLLFI 363
 DB 249 LSVIPTDLYLKGNVPEIRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 308
 QY 364 LHINACVYVWASNYEGITTRWYDGGN-----EYLCRYVAVRTLTITGGPEPQ 415
 DB 309 IHNACVYVFSKAIQFGNDTWYPDVNDPFGRLARKYVSLYSLWSTLTITIGETPPV 368
 QY 416 TLFIVFOLLNFFSGVVFESSLIGMRDVGAAQANQYERACMDTIAVMNYSIPKLV 475
 DB 369 RDSYFFVADFLGLVIFATIGNISMSNNMAARAEFOARLDAIKQWHPFNVSMD 428
 QY 476 QKRYRTWEYTDWSQRLMDSLLKLTPTTTLQALADVNFPSISKVDLFGCDTQMIYD 535
 DB 429 EKRVIKFDYLTWNTKTVDEREVLKLPDKLRABIAINVHLDLTLLKVRIFADCEAGLVE 488

QY 536 MLRLKSLVLYLPQDFVCKKEIGKEMVYIIKHGEVQVLGGPDGKTVLVTIKAGSVFEISL 595
 DB 489 LVVLKLPQVYSPGDIYCKGDIQREMYIIKEGLAVV-ADDGITQFVVLSDGSYFGEISI 547
 QY 596 LAAGG---GNRRNTANVAVGFANLTLTKKTYQELVHYPSERILMKARVLLKQKA-- 650
 DB 548 LNIKSGKAGNRRNTANIKSIGYSDFLCSKDDLMLEALTEYFDAGKMLEEKQKILMKDGLL 607
 QY 651 --KTAEATPRKDALLPKPEETPKLTKTLGGTGKASLARLL-----KLKREQAA 700
 DB 608 DINIAGSDPKLEBEKVTRMESSVLLQOT-----RFAILAEYSMQOKLQRLTK 659
 QY 701 QXK 703
 DB 660 VEK 662
 RESULT 14
 CNMG3_BOVIN
 ID CNMG3_BOVIN STANDARD; PRT; 706 AA.
 AC Q29441;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)
 DE (CNG-3) (CNG3) (Cyclic nucleotide-gated channel alpha 3) (Cone
 DE photoreceptor cGMP-gated channel alpha subunit).
 GN DE
 GN CNGA3 OR CNMG3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Testis;
 RC MEDLINE=94211295; PubMed=7512693;
 RX Weyand I., Godde M., Frings S., Weiner J., Mueller F., Altenhofen W.,
 RA Hatt H., Kaupp U.B.;
 RT "Cloning and functional expression of a cyclic-nucleotide-gated
 RL channel from mammalian sperm."
 RL Nature 368:859-863 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=94224768; PubMed=8170936;
 RA Biel M., Zong X., Distler M., Bosse E., Klugbauer N., Murakami M.,
 RA Flockerzi V., Hofmann F.;
 RT "Another member of the cyclic nucleotide-gated channel family,
 RL expressed in testis, kidney, and heart."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3505-3509 (1994).
 CC -!- FUNCTION: Could be responsible for cGMP-induced calcium entry in
 CC cells other than sensory cells. Might be involved in chemotaxis of
 CC sperm.
 CC -!- SUBUNIT: Forms functional heterooligomeric channels with CNMG3 in
 CC vitro.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Testis, kidney, retinal cone and heart.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; X89600; CAA61759.1; -
 DR EMBL; X76485; CAA54023.1; -
 DR PIR; A55251; A55251.

DR	InterPro; IPR000595; cNMP binding.	
DR	InterPro; IPR005821; Ion_trans.	
DR	InterPro; IPR001632; K-channel_pore.	
DR	Pfam; PF00027; cNMP binding; 1.	
DR	Pfam; PF00520; ion trans; 1.	
DR	SMART; SM00100; cNMP; 1.	
DR	PROSITE; PS00888; cNMP BINDING_1; 1.	
DR	PROSITE; PS00889; cNMP BINDING_2; 1.	
DR	PROSITE; PS00890; cNMP BINDING_3; 1.	
KW	Ionic channel; Ion transport; CAMP-binding; Transmembrane;	
KW	Multigene family; Vision.	
FT	POTENTIAL.	
FT	TRANSMEM 186 206	
FT	TRANSMEM 322 342	
FT	TRANSMEM 398 418	
FT	NP_BIND 501 624	
FT	BINDING 568 588	
FT	BINDING 583 583	
SQ	SEQUENCE 706 AA; 81132 MW; P4990DCD29B56239 CRC64;	
Query Match 18.8%; Score 794; DB 1; Length 706;		
Best Local Similarity 29.7%; Pred. No. 1.7e-38;		
Matches 204; Conservative 141; Mismatches 263; Indels 80; Gaps 19;		
QY	69 IQDKLSKNSGDLTNPDPQNAEPTGVPRKEMDPGKEP-----111	
DB	28 IENGLSRTHLPCEETSSSELQEGIAMETRGIAESRQSFTSQGPTRLSLRIISLRAWSARH 87	
QY	112 -NSPQKPPAPVINEVADQLNLVKEQRTALYKKLVGDLSSPE-----ASQ 163	
DB	88 LHQEDQRPDS--FLERFRGALQEVSR-----ESHVQNVQSQPDPGRGAWL 136	
QY	164 TAKPTAVPPVKESDDKTEHYRLLWFKVKMPLTEYLK--IKLPNSIDSYTDRIYLLW 221	
DB	137 ARNNTNCNNSKDDKAKKE-----KXKKEKKNPKKEKKDSVMDPSSNMYHW 190	
QY	222 L--LLVTLANWNCWTFPLRVPYQYADNIHNLADIICDIIYLDMLFIOPRLQFYR 279	
DB	191 LTVIAVFPVFNW--CLLV-CRACFDELQSEHLMLWLDYSADILYGDMDL--VEARTGFLE 247	
QY	280 GGDIIVDNSRLKHYRTSTRFQDLVASIIPDFICYLFFGFEN--PMFRANRLMKYTSFEFN 338	
DB	248 QGLWMDASRLKHYIQTTLHLKLDVLSVPTDLAYFKLGNVYELFRNLLKLARLEFF 307	
QY	339 HHLESIMDKAYIVRVIRTTGYLFIHLINACVYWNASNYEGITTRWYDGEN-----392	
DB	308 DRTETRTYNPMFRIGNLVYLIILIIHWNACIYFAISKFTGFGTDSWVYVNSNPYGR 367	
QY	393 --EYLCYVAVRTLTITIGLPPQTLFEIVFOLLNPFSGVVFSSLIQOMRDVIGAATA 450	
DB	368 SRKIYSLWSTLTITIGTPPPVDEEYLFVVIDFLVGLVFIATVGNVGSIMNMNA 427	
QY	451 NONYFRACMDDTIAYMNNYIPKLVQKRVRTWYEYTWDSORMLDSDLLKTLPTTTLAL 510	
DB	428 SRAEFQAKIDSIKQYMQFRKVTQDLTRVIRWFDYLVWANKTVDEKVLKSLPDKLAEI 487	
QY	511 AIDVNFSLISKVDLFCQCDQMIYDMLRLKSVLYLPDGFVCKKGKGTGKEMYLIIKHGEVQ 570	
DB	488 AINVELDTLRKRVIFQCEAGLVVLKRPVAFSGEDYICKKGDIGREMYIIKKGKLA 547	
QY	571 VLGGDGTQKVLVTLKAGSVFGEISLLAAGG---GNRTANVAVHGFANLTLTKTLLOEI 627	
DB	548 VV-AEDGITQVVLGDGYSYFGEISILNKGSKSGNRRTAIRSIGYSDLPCLSKDDLMEA 606	
QY	628 LVHYPDSERILMKAR-VLLKQK---AKTAEATPPKDLALLPPKREETPKLFTLLGGT 683	
DB	607 LTEYFEAKALFEKGRQLMKNDLIDELAKAGADPKDI-----BEKVEHLETSIDSL 659	
QY	684 GKASLARLL-----KLKREQAAQKEN 705	
DB	660 -QTRFARLLAEYNATQMKVQRLSQLES 686	
RESULT 15		

CNG3_MOUSE	STANDARD;	PRT;	631 AA.
ID	CNG3_MOUSE		
AC	Q9JUZ8; Q9WV01;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Cyclic-nucleotide-gated cation channel alpha 3 (CNG channel alpha 3)		
DE	(CNG-3) (CNG3) (Cyclic nucleotide gated channel alpha 3) (Cone		
DE	photoreceptor cGMP-gated channel alpha subunit).		
GN	CNGA3 OR CNGB3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=Retina;		
RX	MEDLINE=20273944; PubMed=10813773;		
RA	Hirano A.A., Hack I., Waessle H., Duvoisin R.M.;		
RT	"Cloning and immunocytochemical localization of a cyclic nucleotide-		
RT	gated channel alpha-subunit to all cone photoreceptors in the mouse		
RT	retina.";		
RL	J. Comp. Neurol. 421:80-94(2000).		
RN	[2]		
RP	SEQUENCE OF 95-631 FROM N.A.		
RC	STRAIN=129/Sv;		
RX	MEDLINE=99307448; PubMed=10377453;		
RA	Biel M., Seeliger M., Pfeiffer A., Kohler K., Gerstner A., Ludwig A.;		
RA	Jaisle G., Fauser S., Zrenner E., Hofmann F.;		
RT	"Selective loss of cone function in mice lacking the cyclic		
RT	nucleotide-gated channel CNG3.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 96:7553-7557(1999).		
CC	!- FUNCTION: Visual signal transduction is mediated by a G-protein		
CC	coupled cascade using cGMP as second messenger. This protein can		
CC	be activated by cyclic GMP which leads to an opening of the cation		
CC	channel and thereby causing a depolarization of cone		
CC	photoreceptors.		
CC	!- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	!- TISSUE SPECIFICITY: Prominently expressed in retina.		
CC	!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel		
CC	(TC 1.A.1.5) family.		
CC	!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
EMBL	AJ243933; CAB89685.1; -		
EMBL	AJ238233; CAB42891.1; -		
EMBL	AJ238240; CAB42891.1; JOINED.		
EMBL	AJ238241; CAB42891.1; JOINED.		
MGD	MGI:1341818; Cng3.		
GO	GO:0005221; F:intracellular cyclic nucleotide activated c...; IPI.		
InterPro	IPR000595; cNMP_binding.		
InterPro	IPR005821; Ion_trans.		
Pfam	PF00027; cNMP_binding; 1.		
Pfam	PF00520; ion trans; 1.		
SMART	SM00100; cNMP; 1.		
PROSITE	PS00888; cNMP_BINDING_1; 1.		
PROSITE	PS00889; cNMP_BINDING_2; 1.		
PROSITE	PS00442; cNMP_BINDING_3; 1.		
KW	Ionic channel; Ion transport; CAMP-binding; Transmembrane;		
KW	Multigene family; Vision.		
FT	TRANSMEM 112 133		POTENTIAL.
FT	TRANSMEM 244 264		POTENTIAL.
FT	TRANSMEM 320 340		POTENTIAL.
FT	NP_BIND 423 546		CAMP.
FT	BINDING 490 490		CAMP (POTENTIAL).

```

FT BINDING      505      505      CAMP (POTENTIAL) .
FT CONFLICT    110      110      C -> Y (IN REF. 2) .
FT CONFLICT    157      157      L -> V (IN REF. 2) .
SQ SEQUENCE    631 AA; 72641 MW; 4FA8CD3B9AA3FE6C CRC64;

Query Match
Best Local Similarity 18.6%; Score 788.5; DB 1; Length 631;
Matches 177; Conservative 110; Mismatches 212; Indels 35; Gaps 13;

QY 214 TDRLLVLLVLLVTLA--YNNWCFPIPLRVFPYQADNIHYHLYADIICDIILYDMLFI 271
Db 105 SNNIYCRWLTAALGVFTNW-CLLV-CRACDELOQSEHLTLLWLDYSADVLYVLDML-V 161

QY 272 QPRLQFVRGGDIIIVDSNELRKHRTSTKFDVDAIIIPFDICYLFFGFN-PMFRANRMLX 330
Db 162 RARTGFLSQGLMVRDTKRLWGHYTKTLHFKLDILSLIPTDLAYLKLGVNYPELAFNELLX 221

QY 331 YTSPEFNHLESINDKAYIYRVITTCYLFILHINACVYVWASNYEGIGTTWVYDGE 390
Db 222 FSRLEFFDRTETRTNYPNVFRIGNLVLYLIIHWNACIYFAISKFIGFGTDSWVYPT 281

QY 391 -----GNEYLRCCYYWAVRTLITIGGLPEPQTLFEIVFOLLNFFSGVFSSLIQMR 442
Db 282 SKPEYARLSRKYISLYWSTLTLTIGETPPVVDDEYLFVVIDFLVGLIFATIVGVG 341

QY 443 DVIGATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRMLEDSDLKTL 502
Db 342 SMISNNAPRVFOAKIDSVKQYMQFRKVTXDLKLETRVIRWFDYLVANRKTVDKEVLK 401

QY 503 PTTQLALAIIDVNTSIIISKVLEKGCDDQMIYDMLRLKSVLPLPGDFVCKKGIGREMY 562
Db 402 PDKLAEIAINVHLDLTKKRIFFQDCAGLLEVLVLKRLPTVPSGDIICKKGIDIGREMY 461

QY 563 IIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAG--GNRRTANVVAHGFANLLTL 619
Db 462 IIKGKLAVV-ADGVTQFVVLSDGSYFGEISILNKGSKSGNERTANIRSIGVSDLFCL 520

QY 620 DKTLCEILVHYPPSERILMKAR-VLLKQKAKTAEATPPRKOLALLFPKEETPKLFT 678
Db 521 SKDDLMEALTEYPDAAKALEEKQIILMKONLIDEDLVAARVDTR----DVEEKVEYLES 576

QY 679 LLGGTGKASLARLL-----KLKROA---AOKENSEGGEKEGKEDKOK 721
Db 577 SL-DILOTRFARLLAEYSASQWKLKQRLTRLESQWNERCCGCFSPDRENSSEDASK 629

```

Search completed: June 21, 2004, 10:06:12
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 10:04:22 ; Search time 23 seconds
(without alignments)
1815.887 Million cell updates/sec

Title: US-09-855-828-1

Perfect score: 4234
Sequence: 1 MFKSLTKVVKVPIGNNEN.....PSAEGGBEVLTIIEYKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	818.5	19.3	690	4	US-09-275-252A-19
2	484	11.4	261	4	US-09-275-252A-18
3	412.5	9.7	910	4	US-08-997-685A-2
4	382.5	9.0	749	4	US-08-997-685A-10
5	382	9.0	528	4	US-08-997-685A-4
6	370	8.7	597	4	US-08-997-685A-12
7	368	8.7	506	4	US-08-997-685A-6
8	360.5	8.5	960	4	US-09-694-777A-21
9	349	8.2	987	4	US-09-694-777A-22
10	347.5	8.2	962	4	US-09-694-777A-24
11	345.5	8.2	962	4	US-09-614-480-9
12	345.5	8.2	962	4	US-08-694-777A-3
13	344	8.1	170	4	US-08-358-383C-27
14	337	8.0	988	4	US-10-162-012-12
15	336	7.9	989	4	US-09-694-777A-23
16	335	7.9	988	4	US-08-614-480-2
17	335	7.9	988	4	US-10-162-012-5
18	334	7.9	319	4	US-09-358-383C-22
19	334	7.9	989	4	US-09-694-777A-4
20	317.5	7.5	1159	2	US-08-956-242-13
21	317.5	7.5	1159	3	US-08-351-215-13
22	317.5	7.5	1159	3	US-09-236-012-2
23	317.5	7.5	1159	3	US-09-236-012-4
24	317.5	7.5	1159	4	US-08-358-383C-10
25	317.5	7.5	1159	4	US-09-275-252A-12
26	302.5	7.1	857	4	US-09-275-252A-11
27	294	6.9	888	2	US-08-956-242-4

28	294	6.9	888	3	US-09-351-215-4	Sequence 4, Appli
29	291.5	6.9	1107	4	US-08-358-383C-16	Sequence 16, Appl
30	282.5	6.7	597	4	US-09-275-252A-7	Sequence 7, Appl
31	268.5	6.3	1102	4	US-08-358-383C-36	Sequence 36, Appl
32	266	6.3	126	4	US-08-997-685A-58	Sequence 58, Appl
33	265.5	6.3	129	4	US-08-997-685A-46	Sequence 46, Appl
34	258	6.1	1083	4	US-09-358-383C-2	Sequence 2, Appli
35	257	6.1	1082	4	US-09-336-643A-20	Sequence 20, Appl
36	257	6.1	1083	4	US-09-600-776-2	Sequence 1, Appli
37	257	6.1	1083	4	US-08-343-494-1	Sequence 2, Appli
38	253.5	6.0	1017	4	US-09-600-776-6	Sequence 1, Appli
39	253	6.0	1284	4	US-09-343-494-9	Sequence 6, Appli
40	253	6.0	1284	4	US-09-358-383C-11	Sequence 9, Appli
41	247.5	5.8	126	4	US-08-997-685A-57	Sequence 57, Appl
42	215	5.1	189	4	US-09-358-383C-25	Sequence 25, Appl
43	174	4.1	542	4	US-09-358-383C-5	Sequence 5, Appli
44	167.5	4.0	131	4	US-08-997-685A-45	Sequence 45, Appl
45	165.5	3.9	119	4	US-08-997-685A-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1		US-09-275-252A-19	
; Sequence 19, Application US/09275252A			
; Patent No. 6641997			
; GENERAL INFORMATION:			
; APPLICANT: The Rockefeller University			
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With			
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation			
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof			
; FILE REFERENCE: 018512-082901US			
; CURRENT APPLICATION NUMBER: US/09/275,252A			
; PRIOR FILING DATE: 1999-03-24			
; PRIOR APPLICATION NUMBER: US 09/045,529			
; PRIOR FILING DATE: 1998-03-20			
; PRIOR APPLICATION NUMBER: US 09/054,347			
; PRIOR FILING DATE: 1998-04-02			
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307			
; PRIOR FILING DATE: 1999-03-22			
; NUMBER OF SEQ ID NOS: 42			
; SOFTWARE: Patent in Ver. 2.1			
; SEQ ID NO 19			
; LENGTH: 690			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-275-252A-19			
Query Match			
Best Local Similarity			
Matches 221; Conservative 128; Mismatches 262; Indels 125; Gaps 22;			
QY	5	LTKNVVKVPIGNNENFQSSRRNEEGSHPS	-----NQSQQTAAOEENKGB-----KSL 53
Db	17	VTMNVIVP-----DIKEIRRMENGACSFSEDDSDAYTSESENNENPHARGSPYSKSL 71	
QY	54	MTKSTPTVTSSEPHNIQDKLSKNSSGDLTNPDPQNAAEPTGTVPPEKEMDFGKEGPN 113	
Db	72	R-KGSPSQREQYLPGAIAIFNVANSS-----NKD-----QEPPEKKKKKKKKKSDXNE 121	
QY	114	PQNKPRAAPVINEYADALQHLNLMKRMORTALYKKLVGDLSSPEASPTAKTAVPPV 173	
Db	122	NNNTP-----KKKKKKKKKK-----E 141	
QY	174	KESDDKPTHEHYRLWLPKVKOMPLTEYLKRIKLPNSIDSYDRLYLWLLVTL--AYNW 231	
Db	142	EKSXDKKEHH-----KKEVV-----IDP--SGNTYNNWLPFCITLPPVNW 180	
QY	232	NCWFILRLVPPYOTADNIHVMFIADICDIIVLYDMLFIQPLQFVRGGDIIVDSNEAR 291	
Db	181	T--MVIAPACDELOSDYLEWILDIIVSDIVILDM--FVTRTGTGLEQLVKEELKI 237	

QY 292 KHYRSTKQDVASIIPDICYLFFGFN-PMFRANRMLKYTSFFPFNHLESIMDKAYI 350
 Db 238 NKYSKQLKDLVLSIPTDLLYFKLWNYPEIRLNRLLSRSMFEFFQRTETRTNYPNI 297
 QY 351 YVIRTTGGLLILHINACVYTWASNYSGIGTRWY-----DGE-----GNEYLRCCYYWAV 402
 Db 298 FRISNLVYVIVIIHWNACVFSISKAGFGNDTWVYPIINDPEFRGLARKYVYSLYWST 357
 QY 403 RLITITIGLPEPQTLEFIVFOLLNFFSGVVFSSLIGOMRDVIGATATONVFRACMDT 462
 Db 358 LTLITIGETPPVRDSEYVVFVVDLGLVLPATVGNIGSMISNNNARAEFQARIDAI 417
 QY 463 IAYMNYISPKLVQKVRTRTWBYTWDORSMLDESLLKTLPTTVOLALADVNFSSIIISKV 522
 Db 418 KQMHFRNVSKDMKRVIKWFDYLTNKKTVDEKEVLKYLDPKLRARAEIATNVLHDLTKKV 477
 QY 523 DLFKGCDDTQMIYDMLRLKSLVLYLPQDFCKVCKGEIGKEMWIIKGEVQVGLGPGDKVLY 582
 Db 478 RIFADCEAGLLVELVKLPQVYSPGDYICKRGDIGREMYIIKGEKLAUV-ADGGVTOFV 536
 QY 583 TLKAGSVFGEISLLAAGG---GNRRTANVVAHGFANLLTLDKTKLQELVHYPPSERILM 639
 Db 537 VLSGSGTTFGEISILNIKSGKAGNRRTANIKSGYSDFLCFLSKDDLMEALTEYPPDAKTMLE 596
 QY 640 KQARVLLKQKA-----KTAERTPPKDLALLPFPKEETPKLFTLLGGTGKASLARLL--- 692
 Db 597 EKGQILMKOGLLDLNIANAGSDPKDSEKVRMEGSDLLQT-----RFAILAEY 648
 QY 693 -----KLXREQAAQK 703
 Db 649 ESMQOKLQRLTKVEK 664
 RESULT 2
 US-09-275-252A-18
 ; Sequence 18, Application US/09275252A
 ; Patent No. 6641997
 ; GENERAL INFORMATION:
 ; APPLICANT: Mackinnon, Roderick
 ; APPLICANT: The Rockefeller University
 ; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
 ; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
 ; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
 ; FILE REFERENCE: 018512-002901US
 ; CURRENT APPLICATION NUMBER: US/09/275,252A
 ; CURRENT FILING DATE: 1999-03-24
 ; PRIOR APPLICATION NUMBER: US 09/045,529
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: US 09/054,347
 ; PRIOR FILING DATE: 1998-04-02
 ; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
 ; PRIOR FILING DATE: 1999-03-22
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 261
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-275-252A-18

Query Match 11.4%; Score 484; DB 4; Length 261;
 Best Local Similarity 37.2%; Pred. No. 7e-35;
 Matches 97; Conservative 58; Mismatches 94; Indels 12; Gaps 4;
 QY 370 VYVWASNYEGIGTRWY-----DGE-----GNEYLRCCYYWAVRLITIGLPEPQTLEFIV 421
 Db 1 IYVAISKIGFVDVTWYFNITPEVGYLAREVIYCLYWSLTLTITIGTPPPVDEEVL 60
 QY 422 FOLLNFFSGVVFSSLIGOMRDVIGATATONVFRACMDDTIAYMNYISPKLVQKVRTR 481
 Db 61 FVIFDELIGLIFATVGNVGSIMNNATRAEFOAKIDAVKHYMQFRKVSKGMEAKVIR 120

QY 482 WYEVWDSORMLDESLLKTLPTTVOLALADVNFSSIIISKVDLFKGCDDTQMIYDMLRLK 541
 Db 121 WFDYLTNKKTVDERILKMLPKLRARAEIATNVLHDLTKKVRIFHDCEAGLLVELVKLR 180
 QY 542 SVLYLPQDFCKVCKGEIGKEMWIIKGEVQVGLGPGDKTKVLYTLKAGSVFGEISLLAAGG- 600
 Db 181 PQVSPGDYICKRGDIGKEMWIIKGEKLAUV-ADGGVTOVALLSAGSCFGEISILNIKGS 239
 QY 601 --GNRRTANVVAHGFANLLTL 619
 Db 240 KGNRRRTANIRSLGYSDDLFLCL 260
 RESULT 3
 US-08-997-685A-2
 ; Sequence 2, Application US/08997685A
 ; Patent No. 6551821
 ; GENERAL INFORMATION:
 ; APPLICANT: The Trustees of Columbia University
 ; APPLICANT: Kandel, Eric
 ; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
 ; FILE REFERENCE: 0575/54806
 ; CURRENT APPLICATION NUMBER: US/08/997,685A
 ; CURRENT FILING DATE: 1997-12-12
 ; NUMBER OF SEQ ID NOS: 60
 ; SOFTWARE: Patent In version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 910
 ; TYPE: PRT
 ; ORGANISM: mouse
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (130)..(148)
 ; OTHER INFORMATION: S1
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (164)..(185)
 ; OTHER INFORMATION: S2
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (208)..(229)
 ; OTHER INFORMATION: S3
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (243)..(271)
 ; OTHER INFORMATION: S4
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (291)..(313)
 ; OTHER INFORMATION: S5
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (332)..(358)
 ; OTHER INFORMATION: P
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (367)..(387)
 ; OTHER INFORMATION: S6
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (472)..(602)
 ; OTHER INFORMATION: CNB
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: AAC53518
 ; DATABASE ENTRY DATE: 1997-12-27
 ; RELEVANT RESIDUES: (1)..(910)
 ; US-08-997-685A-2

Query Match 9.7%; Score 412.5; DB 4; Length 910;
 Best Local Similarity 20.2%; Pred. No. 1.1e-27;
 Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps 25;
 QY 210 IDSYTD-RLVLLMLLVTLAYNWCWFIPLRLPPYQTDNIHVLADIICDIYLYDM 268


```
Db 124 IHPYSDFRFY--WDLIMLMVGNLVIIPVGITF--FTEQTTTFWIFNVASDTVFLLDL 179
QY 269 LFIQRLQFVRG-----GDIIVDSNELRKHYRTSTKFQDVASIIPFDICYL----- 315
Db 180 I-----MNFRTGTVNEDESSEIILDPKVMNLYKSM--FVVDFTSSIPVDYIFLIVEKGM 233
QY 316 -----FFGFENFRANRMLKYTSFPEFNHLESIMDKAY-----IYRVITTYG 359
Db 234 SEVYKTARALIRVFTKILSLRLRLRLIRYTHOWEEIFHMTYDLASAVRIFNLGM 293
QY 360 LFIILHINACVY-----WASNYEGIGTTRWYVDGEGNEYLRCYVAVRTLIT 407
Db 294 MLLCHWDGCLQFLVLLQDPDPDCWVSLNE-----WVDSMGKQVSYALFKAMSHMLC 347
QY 408 IG-GLPEPQTLFEIVFOLLNFFSGVFVSSLIQOMRDVIGAAATANQNYFRACMDDTIAYM 466
Db 348 IGYGAQAPVMSDMLWITMLSNIVGATCYAMFVGHATALIOSLSSRRQYOEKQKQVEQYM 407
QY 467 NNYISPKLVQKRVRTWYETWDSQRMLEDSDLLKTLPTTVQLALADVNFS-----IISKVD 523
Db 408 SFHKLPAQMRQKIHDIYEHRYQG-KIFDEENILSELNDPLREBI--VNFNCRKLVATMP 463
QY 524 LFKGCDTQMIYDMLRLKSVLYLPDGFVCKKGIGKEMYLKKEGVQVLGGPGTKVLVT 583
Db 464 LFANADPNFVTAMLSKURFEVQFGDYIIRREGAVGKMYFIQHGAVGI-----TKSKE 518
QY 584 LKA--GSVFGESISLAAGGNRRRTANVAHGFANLLTLDKKTLOEILVHYPDSEI----- 636
Db 519 MKLTDGSYFGIEICLLTKG--RRTASVRADTYCRLYSLSDVNEFNEVLEEYPMRRAFETV 575
QY 637 -----ILMKK-----ARVLLKQKAK----- 651
Db 576 AIDRLDRIGKNSILLQKQFQDLNTGVNQNENILKQIVKHDRMVQALIPPYQMTA 635
QY 652 ---TAEATPPRKDL-----ALLFP-----P 668
Db 636 LNCSTSTTPTRMRTQSPVYATSLSHSNLHSPSPSTQTPOPSAILSPCSYTTAVCSP 695
QY 669 KEETPKLFTLLGGTKASLARILKLRQAAQ---KKENSEGEBEKEKEDKQENED 725
Db 696 PIQSPLATRTHYASPTASQSLSLQPPQQLPQSQVQQTQTTQOQQQQQQQQQQQQQQQ 755
QY 726 KQKNEDEKGENEDKGRPEEPKPLDRPECTAPIAVEBEHPSVRRTVLPRTGTSQSL- 784
Db 756 QQQQQQQQQQQQQQQQQQQQQQQTGSSSTPKNEVHKSTQALHNTLNLIKVEPLSASQPSUP 815
QY 785 -----IISMAFSAGGEBVLTI 801
Db 816 HEVSTLIS-RPHPTVGESLASI 836

RESULT 4
US-08-997-685A-10
; Sequence 10, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 749
; TYPE: PRT
; ORGANISM: human
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC399759
; DATABASE ENTRY DATE: 1998-05-29
; RELEVANT RESIDUES: (1)..(749)
```

```
US-08-997-685A-10
Query Match
Best Local Similarity 9.0%; Score 382.5; DB 4; Length 749;
Matches 119; Conservative 99; Mismatches 196; Indels 87; Gaps 18;

QY 210 IDSYTD-RLYLLWLLLLVLAANNWCFILRLRFPVQTDADNIHYWLIADIICDIIVLYDM 268
Db 14 IHPYSDFRFY--WDLIMLMVGNLVIIPVGITF--FTEQTTTFWIFNVASDTVFLLDL 69
QY 269 LFIQRLQFVRG-----GDIIVDSNELRKHYRTSTKFQDVASIIPFDICYL----- 315
Db 70 I-----MNFRTGTVNEDESSEIILDPKVMNLYKSM--FVVDFTSSIPVDYIFLIVEKGM 123
QY 316 -----FFGFENFRANRMLKYTSFPEFNHLESIMDKAY-----IYRVITTYG 359
Db 124 SEVYKTARALIRVFTKILSLRLRLRLIRYTHOWEEIFHMTYDLASAVRIFNLGM 183
QY 360 LFIILHINACVY-----WASNYEGIGTTRWYVDGEGNEYLRCYVAVRTLIT 407
Db 184 MLLCHWDGCLQFLVLLQDPDPDCWVSLNE-----WVDSMGKQVSYALFKAMSHMLC 237
QY 408 IG-GLPEPQTLFEIVFOLLNFFSGVFVSSLIQOMRDVIGAAATANQNYFRACMDDTIAYM 466
Db 238 IGYGAQAPVMSDMLWITMLSNIVGATCYAMFVGHATALIOSLSSRRQYOEKQKQVEQYM 297
QY 467 NNYISPKLVQKRVRTWYETWDSQRMLEDSDLLKTLPTTVQLALADVNFS-----IISKVD 523
Db 298 SFHKLPAQMRQKIHDIYEHRYQG-KIFDEENILSELNDPLREBI--VNFNCRKLVATMP 353
QY 524 LFKGCDTQMIYDMLRLKSVLYLPDGFVCKKGIGKEMYLKKEGVQVLGGPGTKVLVT 583
Db 354 LFANADPNFVTAMLSKURFEVQFGDYIIRREGAVGKMYFIQHGAVGI-----TKSKE 408
QY 584 LKA--GSVFGESISLAAGGNRRRTANVAHGFANLLTLDKKTLOEILVHYPDSEI----- 637
Db 409 MKLTDGSYFGIEICLLTKG--RRTASVRADTYCRLYSLSDVNEFNEVLEEYPMRRAFETV 465
QY 638 -----LMKKARVLLKQKAK 651
Db 466 AIDRLDRIGKNSILLQKQFQDLNTGVNQNENILKQIVKHDRMVQALIPPYQMTA 635

RESULT 5
US-08-997-685A-4
; Sequence 4, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 528
; TYPE: PRT
; ORGANISM: mouse;
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AAC40125
; DATABASE ENTRY DATE: 1998-05-29
; RELEVANT RESIDUES: (1)..(504)
US-08-997-685A-4

Query Match
Best Local Similarity 9.0%; Score 382; DB 4; Length 528;
Matches 129; Conservative 95; Mismatches 213; Indels 92; Gaps 20;

QY 202 KRIKLPNS--IDSYTD-RLYLLWLLLLVLAANNWCFILRLRFPVQTDADNIHYWLIADI 256
Db 18 ERVKSAGAWIHPYSDFRFY--WDLIMLMVGNLVIIPVGITF--FTEQTTTFWIFNVASDTVF 71
```


; ORGANISM: Mus sp.	
US-09-694-777A-23	
Query Match 7.9%; Score 336; DB 4; Length 989;	
Best Local Similarity 19.7%; Pred. No. 8.5e-21;	
Matches 126; Conservative 113; Mismatches 242; Indels 158; Gaps 23;	
Qy	221 WLLVLTAYNNCWFIPLRLVFPY-----QTADNIHYWLIADIICDIIYLYDML-----F 270
Db	222 WIIILITFTY-----AIIYPYNSFKTRQNNVAVLVDSIVDVIPLVDIVLNFHTTF 273
Qy	271 IQPRLQFVGGDIIIVDSNELRKHRTSTKFDLVASIIIPDICYLP----- 316
Db	274 VGP-----AGEVISDPKLRMNY-LKTFWVIDLLSCLPYVINAFENVDEVSAFMGDEG 326
Qy	317 -PGF-----NPMFRANMLKVTSPF-----EFNHLESIMDKAYIYRVIR 355
Db	327 KIGFADQIIPPLEGRESQGISSLFSLKVVRLRLGRVARKLDHYIE--YGAIVLVLC 384
Qy	356 TCGYLLFILHINACVYWNASNYE-----GIGTTRWVY-----DQEG----- 391
Db	385 VFG---LAAHWMACIWSYIGDYEIFDEDTKTIRNSWLYQLALDICTPYQFNGSGSGKE 441
Qy	392 -----NEYLRCYVWVRTLTITIG-GLPEPQTLFEIVFOLLNFFSGVFVFSLLIGOMRDV 444
Db	442 GSPSKNSVIISLYFTMTSLTSVGFGNIAPISTDIKIFAVAINMIGSLIYATIFGNVTI 501
Qy	445 IGAATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRMDESLLKTLPT 504
Db	502 FQQMYANTNRYHEMLNSVRDFLKLQVPKGLSERVMDYIVSTWSMRGIDTEKVLQICPK 561
Qy	505 TVQLALAIQVNFIIISKVDLPKGCDDTQMIYDMLRLKSLVLYLEGDFVCKKGEIGKEMYII 564
Db	562 DMRADICVHLNRKVFKEHPAFRLASDGLRALAMEFQTVHCAPGDIIYHAGESVDSLQFV 621
Qy	565 KHGEVQVLGGPDGTQVLVTLKAGSVFGEI-----SLLAAGGGRNRTANVVAHGFANLLTLD 620
Db	622 VSGSLEVI---QDDEVVAIIKGEDVGDVFWKEATLA---QSCANVRALTYCDLHLVIK 673
Qy	621 KKTLOEILVHYPD-----SERILMK---KARVLLKO-----KAKTAEATPPKDLALLPPP 668
Db	674 RDAIQLVLEFYTAFSHSFSRNLITVNLKRIIVFRKISDVKREEBEEMKRNKNEAPLILPP 733
Qy	669 KEETPKLPKTLIGGTGKASLARLLKLRBOAAOKKENSEGEGEEGKENEKQKENEKQK 728
Db	734 DHPVRLUF-----QFRQCKEARLAAERGGRLDLDLVE----- 767
Qy	729 ENEDKGENEDKQKREPEEKPLDRPECTASPIAVEEEP 767
Db	768 ---KGNALTDHTSANHGLAK-----ASVTVRESP 794

Search completed: June 21, 2004, 10:08:25
Job time : 26 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 21, 2004, 10:07:22 ; Search time 49 Seconds
(without alignments)
4661.056 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSLTKVANKVPIGENNEN.....PSAEGGEVLTIVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PTCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PTCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	906	21.4	237	15	US-10-189-507-11
2	902	21.3	237	15	US-10-189-507-7
3	850	20.1	694	10	US-09-842-758-75
4	850	20.1	694	12	US-10-174-333-75
5	850	20.1	694	14	US-10-345-680-26
6	829	19.6	663	14	US-10-029-677-16
7	825.5	19.5	664	14	US-10-029-677-24
8	820.5	19.4	664	14	US-10-029-677-2
9	820	19.4	732	10	US-09-842-758-73
10	820	19.4	732	12	US-10-174-333-73
11	820	19.4	732	14	US-10-029-677-15
12	819.5	19.4	664	9	US-09-735-927-2
13	819.5	19.4	664	13	US-10-034-843-2
14	819.5	19.4	664	14	US-10-168-651-7
15	819.5	19.4	664	14	US-10-114-153-18

16	818.5	19.3	664	9	US-09-735-927-4
17	804	19.0	664	14	US-10-029-677-18
18	804	19.0	664	14	US-10-087-217-2
19	804	19.0	664	14	US-10-295-573-8
20	802	18.9	664	14	US-10-295-573-5
21	795	18.8	664	14	US-10-087-217-4
22	791	18.7	664	14	US-10-087-217-6
23	791	18.7	664	14	US-10-295-573-6
24	782	18.5	664	14	US-10-087-217-8
25	777.5	18.4	664	14	US-10-029-677-17
26	773	18.3	634	14	US-09-842-758-28
27	656	15.5	578	10	US-09-842-758-28
28	656	15.5	578	12	US-10-174-333-28
29	655	15.5	575	9	US-09-735-932-2
30	655	15.5	575	9	US-09-927-267-1
31	655	15.5	575	10	US-09-842-758-30
32	655	15.5	575	12	US-10-174-333-30
33	655	15.5	575	14	US-10-207-951-2
34	640	15.1	575	9	US-09-735-932-4
35	640	15.1	575	9	US-09-927-267-16
36	640	15.1	575	10	US-09-842-758-74
37	640	15.1	575	12	US-10-174-333-74
38	450.5	10.6	239	15	US-10-189-507-5
39	449.5	10.6	239	15	US-10-189-507-9
40	437	10.3	239	15	US-10-189-507-12
41	430	10.2	103	9	US-09-911-826A-25
42	413	9.8	1203	14	US-10-067-457-3
43	413	9.8	1245	12	US-10-276-774-2323
44	412.5	9.7	910	10	US-09-086-436-31
45	412.5	9.7	1203	12	US-10-311-795-6

ALIGNMENTS

RESULT 1

US-10-189-507-11
; Sequence 11, Application US/10189507
; Publication No. US20030228633A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: MOYER, BRYAN
; APPLICANT: PRONIN, ALEX
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: SERVANT, GUY
; APPLICANT: CALLAMARAS, NICHOLAS
; TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
; TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
; TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
; TITLE OF INVENTION: SMELL MODULATORS
; FILE REFERENCE: 078003-0291567
; CURRENT APPLICATION NUMBER: US/10/189,507
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/303,140
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/337,154
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-507-11

Query Match 21.4%; Score 906; DB 15; Length 237;

Best Local Similarity 72.8%; Pred. No. 9.6e-62;
Matches 171; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

QY 417 LFEIVFQLNFFSGVFFSSLIQMDVIGATFANQYFRACMDDTIAYNNYSIPKLVQ 476

Db 1 LFEIVFOLLNFTGTFVAFSVMIGQMRDVGAAATAGCTYRSCMDSTVKYMMFYKIPKSVQ 60
 QY 477 KRVRTWYETWDSQRMDESDLLKTLPTTQVLAALDAIDVNFSTIISKVDLFGKCDTQMIYDM 536
 Db 61 NRKVTWYETWHSQGMDESELMVOLPDKMRDLDAIDVNYIVSKVALFGQCDRQMIFDM 120
 QY 537 LLRLKSVLYLPDGFVCKKGEIKEMVYIKHGEVQVLGGPDGTVKVLVTLKAGSVFGISLL 596
 Db 121 LKRLSVVLYLPNDYVCKKGEIGREMYIIQAGQVQVLGGPDGKSVLVTLKAGSVFGISLL 180
 QY 597 AAGGNRRRTANVVAHGFANLLTLDKKTQELVHYPDSERILMKKARVLLKQAK 651
 Db 181 AVGGNRRRTANVVAHGFTNLFILDKDLNEILVHYPESQKLLRKARMLRNNK 235

RESULT 2

US-10-189-507-7
 ; Sequence 7, Application US/10189507
 ; Publication No. US20030228633A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZOLLER, MARK
 ; APPLICANT: XU, HONG
 ; APPLICANT: STASZEWSKI, LENA
 ; APPLICANT: MOYER, BRYAN
 ; APPLICANT: PRONIN, ALEX
 ; APPLICANT: ADLER, JON ELLIOT
 ; APPLICANT: SERVANT, GUY
 ; APPLICANT: CALLAMARAS, NICHOLAS
 ; TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
 ; TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
 ; TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
 ; TITLE OF INVENTION: SWEET MODULATORS
 ; FILE REFERENCE: 078003-0291567
 ; CURRENT APPLICATION NUMBER: US/10/189,507
 ; CURRENT FILING DATE: 2003-02-12
 ; PRIOR APPLICATION NUMBER: 60/303,140
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 60/337,154
 ; PRIOR FILING DATE: 2001-12-10
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 237
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 US-10-189-507-7

Query Match 21.3%; Score 902; DB 15; Length 237;
 Best Local Similarity 72.3%; Pred. No. 2e-61;
 Matches 170; Conservative 30; Mismatches 35; Indels 0; Gaps 0;
 QY 417 LFEIVFOLLNFTGTFVAFSVMIGQMRDVGAAATAGCTYRSCMDSTVKYMMFYKIPKSVQ 476
 Db 1 LFEIVFOLLNFTGTFVAFSVMIGQMRDVGAAATAGCTYRSCMDSTVKYMMFYKIPKSVQ 60
 QY 477 KRVRTWYETWDSQRMDESDLLKTLPTTQVLAALDAIDVNFSTIISKVDLFGKCDTQMIYDM 536
 Db 61 NRKVTWYETWHSQGMDESELMVOLPDKMRDLDAIDVNYIVSKVALFGQCDRQMIFDM 120
 QY 537 LLRLKSVLYLPDGFVCKKGEIKEMVYIKHGEVQVLGGPDGTVKVLVTLKAGSVFGISLL 596
 Db 121 LKRLSVVLYLPNDYVCKKGEIGREMYIIQAGQVQVLGGPDGKSVLVTLKAGSVFGISLL 180
 QY 597 AAGGNRRRTANVVAHGFANLLTLDKKTQELVHYPDSERILMKKARVLLKQAK 651
 Db 181 AVGGNRRRTANVVAHGFTNLFILDKDLNEILVHYPESQKLLRKARMLRNNK 235

RESULT 3

US-09-842-758-75
 ; Sequence 75, Application US/09842758
 ; Publication No. US20030083244A1
 ; GENERAL INFORMATION:

; APPLICANT: Vernet, Corine A. M.
 ; APPLICANT: Fernandes, Elma R.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Majumder, Kumud
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Padicaru, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Gangolli, Esha A.
 ; APPLICANT: Smithson, Glennda
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Edward, Szekeres S.
 ; APPLICANT: Alsodbrook II, John P.
 ; TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-783
 ; CURRENT APPLICATION NUMBER: US/09/842,758
 ; CURRENT FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: 60/200,158
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: 60/200,613
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,780
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/201,006
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,007
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,236
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,238
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,186
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,474
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/201,508
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/220,591
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: 60/232,678
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: 60/263,217
 ; PRIOR FILING DATE: 2001-01-22
 ; PRIOR APPLICATION NUMBER: 60/265,160
 ; PRIOR FILING DATE: 2001-01-30
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 75
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-842-758-75

Query Match 20.1%; Score 850; DB 10; Length 694;
 Best Local Similarity 30.0%; Pred. No. 9.7e-57;
 Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;
 QY 27 NEEGHPNQSQTTAQENKGEKSLKSTPTVTSBEPHTNIQDKLSKKNSSGDLTNP 86
 Db 5 NTQYSHPS-----RTHLKVK-----TSORDLNRAENGLSRAHSSEETS-- 43
 QY 87 DPQNAEPTGTVPQKEMDPKQEGNSPQKPPAPVINEYADQALHNLVKKRQRTALY 146
 Db 44 ---SVLQP-GIAMETRGGLADSGQSGFTGQ-----GIARLRLIFLLRWAARH 87

```

QY 147 KKKLVEGDLSSP-----EASPTAKPTAVPPVKESDDKPTHEHYRLLWFKVKMPL 197
Db 88 VHQDQGPSDFPRFGAELKEVSSQESNAQAVGQEPADRG-----RSAM-----PL 136
QY 198 -----TEYLKRIKLPSNI-DSYTDRLYLMLLVTLAYNNWNCWPIPLRLVPYQT 246
Db 137 AKCNTNTSNTTEEEKTKKDAIVDPSSNLYRWLTAIALPVPYNNWLLICRACFDELQ 196
QY 247 ADNIHWLIADICDIILYDMLFIQPRLOFVRGGDIIVDSNELRKHVYRTSTKFOLDVAS 306
Db 197 SEYLMWLVLVDYSADVLVLDVL-VRAATGFLQGLMVSQDNLWQHXYKTTQFKLDVLS 255
QY 307 IIPFDICYLFFGFN-PMFRANRMLKXTSPFENHLESIMDKAYIRVIRTTGYLLFILH 365
Db 256 LVPTDLAYLVKVTNYPEVEFNLLKFSRLEFFDRTETRTNYPNMFRIGNLVLYLIIH 315
QY 366 INACVYVWASNYEGIGTRWVDG-----EGNEYLRCYYWAVRVLITIGGLPPQTL 417
Db 316 WNACIVFAISKFGTDSWYFNISIPBHGRLSRKYVLSYVSTLTLTIGETPPVKD 375
QY 418 FEIVFOLLNFFSGVFFVSSLIQOMRDVIGAATANQNYFRACMDTIAYNNYSIPKLVK 477
Db 376 EYLVFVVVDPLVGLVLIFAIVGVSMISNNWASRAEFQAKIDSIRQYMQFRKVTKDLET 435
QY 478 RVRTWYETWDSQRMDESDLLKTPTTVQLALADVNFISIISKVDLFGKCDTQMIVDML 537
Db 436 RVIRWFDYLWANKKTVDKEVLSLDPDKLAEIAINVHLDTLKARIFQDCEAGLVELV 495
QY 538 LRLKSLVLYLFGDFCKYGEIGKEMYYIKHGEVQVGLGPDGKTVLTLKAGSVFGEISILA 597
Db 496 LKLRPTVFSGDYICKGDIKGEMYLINECKLAVV-ADGVTQVVLSDGSYFGEISILN 554
QY 598 AGG---GNRTANVAVHGFANLTLTKKTLOBLVHPDSEIRLMKKAR-VILKQK---A 650
Db 555 IKGSKGNRRNTANIRSIGYDLFCLSKDLMEALTEYPEAKKALEEKGRIKMLKNDLIDE 614
QY 651 KTEATPRKDLALLFPKZETPKLFTLLGGTGKASLARLL-----KLKREOAAQK 702
Db 615 ELARAGADPKDL-----EKVEQLGSSL--DTLQTFALLAEYNATQMKQRISQLE 666
QY 703 KENSEGEE---EGKENEDKQKENEKQK 728
Db 667 SQVKGKGDPLADGEVPGDATK-TEDKQK 694

```

RESULT 4

```

US-10-174-333-75
; Sequence 75, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine B.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li

```

```

; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 75
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-174-333-75

```

Query Match 20.1%; Score 850; DB 12; Length 694;

Best Local Similarity 30.0%; Pred. No. 9.7e-57;

Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

```

QY 27 NEEGSHPNQSQTTAAQENKGEEXSLTKSPVTSSEPHNTNIQKLSKQSSGDLTNP 86
Db 5 NTQYSHPS-----RTHLVK-----TSDRLNEAENGLSRAHSSSETS-- 43
QY 87 DPONAAEPTGVPEQKEMDPGKGNPSQNKPPAAPVINEYADAOHLNVLKMRORTALY 146
Db 44 ---SVLQP-GIAMETRGADSGQSGFTGQ-----GIARLSLIFLLRWAARH 87
QY 147 KKKLVEGDLSSP-----EASPTAKPTAVPPVKESDDKPTHEHYRLLWFKVKMPL 197
Db 88 VHQDQGPSDFPRFGAELKEVSSQESNAQAVGQEPADRG-----RSAM-----PL 136
QY 198 -----TEYLKRIKLPSNI-DSYTDRLYLMLLVTLAYNNWNCWPIPLRLVPYQT 246
Db 137 AKCNTNTSNTTEEEKTKKDAIVDPSSNLYRWLTAIALPVPYNNWLLICRACFDELQ 196
QY 247 ADNIHWLIADICDIILYDMLFIQPRLOFVRGGDIIVDSNELRKHVYRTSTKFOLDVAS 306
Db 197 SEYLMWLVLVDYSADVLVLDVL-VRAATGFLQGLMVSQDNLWQHXYKTTQFKLDVLS 255
QY 307 IIPFDICYLFFGFN-PMFRANRMLKXTSPFENHLESIMDKAYIRVIRTTGYLLFILH 365
Db 256 LVPTDLAYLVKVTNYPEVEFNLLKFSRLEFFDRTETRTNYPNMFRIGNLVLYLIIH 315
QY 366 INACVYVWASNYEGIGTRWVDG-----EGNEYLRCYYWAVRVLITIGGLPPQTL 417
Db 316 WNACIVFAISKFGTDSWYFNISIPBHGRLSRKYVLSYVSTLTLTIGETPPVKD 375
QY 418 FEIVFOLLNFFSGVFFVSSLIQOMRDVIGAATANQNYFRACMDTIAYNNYSIPKLVK 477
Db 376 EYLVFVVVDPLVGLVLIFAIVGVSMISNNWASRAEFQAKIDSIRQYMQFRKVTKDLET 435
QY 478 RVRTWYETWDSQRMDESDLLKTPTTVQLALADVNFISIISKVDLFGKCDTQMIVDML 537
Db 436 RVIRWFDYLWANKKTVDKEVLSLDPDKLAEIAINVHLDTLKARIFQDCEAGLVELV 495

```


Db 3 EKANGVKSPANNHHPAIPAKSGD---DHRASSRPQSAADDTSSQLQLAEMDAP 59

QY 108 KEGPNSPQKPPAPVINYA-----DAQHNLVKRMQRTALYKKLVGEGDLSDEA 160

Db 60 QQRGGFRRIARLVGLVREWAYRNFREBPRPDSFLERF-----GPEL 103

QY 161 SPQAKTAPVPPVKESDDKPTHEHYRLWFKVKOMPLTEYLKRIKLPNISIDSYTRLVLL 220

Db 104 HTVTTQGGKGDGOGEGKTKKFFLF-----VLDPAGD-WYR 142

QY 221 WLLLVTL--AYNWCWFILRLVFPYQTADNIHNLADIICDIYLYDMLFIQRLQV 278

Db 143 WLFVAMPVLVNW-CLLV-ARACFSDLOKGYIYVWLVVDVSDVVIAD-LFIRLTGFL 199

QY 279 RGGDIIVDSNELKRYRTSTKFDLVASIIIPEDICYLFPGF-NPMFRANRLKYSFPF 337

Db 200 EQGLLVKDTKLRDNYIHTLOFKLDVASIIPDIIYPAVDIHSPEVRNRLHFAFMFEF 259

QY 338 NHLESIMDKAYIYRVIRITGTYLLFILHINACVYVWASNYEGIGTRVWY----DGE--- 390

Db 260 FDTETRTSYNIFRISNLVLIYIIHWNACIYVIAISKISGFGVDTWVYVNIIDPEYGY 319

QY 391 -GNEYLRVYVAVRVLITIGGLPEPOTLFEIVFOLLNFFSGVVFSSLIQMRDVIGAAT 449

Db 380 ATRAEFQAKIDAVKHYMQFRKVKMEAKVIRWFDVLTNKKSVDEREVLKNIPLAKRAE 439

QY 510 LAIDVNFISIISKVDLFKGCDDTOMYDMLRLKSVLPLGDFVCKKGEIGKEMVYIKHGEV 569

Db 440 IAINVHLSTLKVRIQDCEAGLLVELVILKURPQVSPGDIYICRKGDIKEMVYIKHGEV 499

QY 570 QVLLGGPDGKVLVTLKAGSVFGEISLLAAG--GNERTANVVAHGFANLLTLDKKTLOE 626

Db 500 AVV-ADDGVTQYALLSAGSCFGEISILNIGSKMGNRRTANIRSLGSDVFCLSKDLME 558

QY 627 ILVHYDSEIRILMKARVLLKQAKTAE---ATPPKDLALLFPPEETPKLTKLGGT 683

Db 559 AVTEYPAKVLIERGRELKMEGLLDENEVAASMEVDV-----QELKQLETNM--DT 610

QY 684 GKASLALLKLRQAAQKENSEGGEKEDKOKEN--EDKOKENEDKEDKEDKD 741

Db 611 LYTRFARLL-----AETGAQOKLKQRTITVLETKMKNNEDDLSOGMN 654

QY 742 KGRPEEPK 750

Db 655 SPEPPAEK 663

RESULT 7

US-10-029-677-24

; Sequence 24, Application US/10029677

; Publication No. US20030096249A1

; GENERAL INFORMATION:

; APPLICANT: Westphal, Ryan S.

; APPLICANT: Feder, John N.

; APPLICANT: Ramanathan, Chandra S.

; APPLICANT: Mintier, Gabriel A.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL

; TITLE OF INVENTION: POLYPEPTIDE

; FILE REFERENCE: D0187NP

; CURRENT APPLICATION NUMBER: US/10/029,677

; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: US 60/257,865

; PRIOR FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: Patent version 3.0

; SEQ ID NO 24

; LENGTH: 664

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-029-677-24

Query Match 19.5%; Score 825.5; DB 14; Length 664;

Best Local Similarity 29.6%; Pred. No. 7.2e-55;

Matches 218; Conservative 129; Mismatches 284; Indels 105; Gaps 21;

QY 50 EKSLTKSTPVTSEPHNTIQQKLSKNSSGDLTTPDQNAABPTQVPEQK--EMDPG 107

Db 3 EKTNGVKSSPANNENHHA--PPAIIKANGKDDHRTSSRPHSAADDTSSLRQADYDAP 59

QY 108 KEGPNSPQKPPAPVINEYADAQLH-----NLVKRMQRTALYKKLVGEGDLSDEA 160

Db 60 QQRGGFRRIARLVGLVREWAYRNFREBPRPDSFLERF-----GPEL 103

QY 161 SPQAKTAPVPPVKESDDKPTHEHYRLWFKVKOMPLTEYLKRIKLPNISIDSYTRLVLL 220

Db 104 QTVTTQGGKGDGOGEGKTKKFFLF-----VLDPAGD-LYIC 142

QY 221 WLLLVTL--AYNWCWFILRLVFPYQTADNIHNLADIICDIYLYDMLFIQRLQV 278

Db 143 WLFVAMPVLVNW-CLLV-ARACFSDLOKGYIYVWLVVDVSDVVIAD-LFIRLTGFL 199

QY 279 RGGDIIVDSNELKRYRTSTKFDLVASIIIPEDICYLFPGF-NPMFRANRLKYSFPF 337

Db 200 EQGLLVKDTKLRDNYIHTLOFKLDVASIIPDIIYPAVDIHSPEVRNRLHFAFMFEF 259

QY 338 NHLESIMDKAYIYRVIRITGTYLLFILHINACVYVWASNYEGIGTRVWY----DGE--- 390

Db 260 FDTETRTSYNIFRISNLVLIYIIHWNACIYVIAISKISGFGVDTWVYVNIIDPEYGY 319

QY 391 -GNEYLRVYVAVRVLITIGGLPEPOTLFEIVFOLLNFFSGVVFSSLIQMRDVIGAAT 449

Db 380 ATRAEFQAKIDAVKHYMQFRKVKMEAKVIRWFDVLTNKKSVDEREVLKNIPLAKRAE 439

QY 510 LAIDVNFISIISKVDLFKGCDDTOMYDMLRLKSVLPLGDFVCKKGEIGKEMVYIKHGEV 569

Db 440 IAINVHLSTLKVRIQDCEAGLLVELVILKURPQVSPGDIYICRKGDIKEMVYIKHGEV 499

QY 570 QVLLGGPDGKVLVTLKAGSVFGEISLLAAG--GNERTANVVAHGFANLLTLDKKTLOE 626

Db 500 AVV-ADDGVTQYALLSAGSCFGEISILNIGSKMGNRRTANIRSLGSDVFCLSKDLME 558

QY 627 ILVHYDSEIRILMKARVLLKQAKTAE---ATPPKDLALLFPPEETPKLTKLGGT 683

Db 559 AVTEYPAKVLIERGRELKMEGLLDENEVAASMEVDV-----QELKQLETNM--DT 610

QY 684 GKASLALLKLRQAAQKENSEGGEKEDKOKEN--EDKOKENEDKEDKEDKD 741

Db 611 LYTRFARLL-----AETGAQOKLKQRTITVLETKMKNNEDDLSOGMN 654

QY 742 KGRPEEPK 750

Db 655 SPEPPAEK 663

RESULT 8

US-10-029-677-2

; Sequence 2, Application US/10029677

; Publication No. US20030096249A1

; GENERAL INFORMATION:

; APPLICANT: Westphal, Ryan S.

; APPLICANT: Feder, John N.

; APPLICANT: Ramanathan, Chandra S.

; APPLICANT: Mintier, Gabriel A.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FOR A HUMAN CATION CHANNEL

; TITLE OF INVENTION: POLYPEPTIDE

; FILE REFERENCE: D0187NP

; CURRENT APPLICATION NUMBER: US/10/029,677

; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: US 60/257,865
 ; PRIOR FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 664
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-029-677-2

Query Match 19.4%; Score 820.5; DB 14; Length 664;
 Best Local Similarity 29.5%; Pred. No. 1.7e-54;
 Matches 217; Conservative 129; Mismatches 285; Indels 105; Gaps 21;
 QY 50 EKSLTKTPTVTSEEPHNTIQDKLSKSSGDLTTPQNAAEPTGTVPQK--EMDPG 107
 DB 3 EKTNGVKSPANNHHA---PPAIKANGKDDHTSSPHSAADDTSSSELQRLADVAP 59
 QY 108 KEGPNSQNKPPAAPVINEYADAQJH-----NLVKMRQRTALYKXKLVGDLSSPEA 160
 DB 60 CQGRSGFRIVRLVGIIRWANKNPREEPDPDFLERF-----GPEL 103
 QY 161 SPQAKTAPVPEKSDDKPTHEHYVRLVFKVKKMPLTEYLKRIKLPNSIDSYDRLYL 220
 DB 104 QTVTQEGDGKDGKDGKXKPELF-----VLDPAQD-LYYC 142
 QY 221 WLLVTL--AYNNCWFFPLRLVFPYQADNIHWLIADIICDIYLYDMLFIQPRLOFV 278
 DB 143 WLFVAMPVLYNW-CLLV-ARACFSDLQGYLVWLVLDVYDVYIAD-LFIRLRTGFL 199
 QY 279 RGGDIIVDSNELKHYRSTFKQDVASIIIPDFCYLFFGF-NMFPANMLKYSFEP 337
 DB 200 EQLLVKDTKLRDNYHTLOKLDVASIIPDTLIYFAVDIHSPEVFNRLHFAFMFE 259
 QY 338 NHLESIMDKAYIVRVIRTTGCLLFIHLINACVYVWASNYEGITRWVY----DGS--- 390
 DB 260 FDRTRTYNPIFRISNLVLYLVIHWNACIYVAISKIGFVDTWVYFNITDPEYGY 319
 QY 391 -GNEVLRYYAVRTLTITIGLBPQTLFEIVFOLLNPFSGVFFSLLIQMRDVIGAAT 449
 DB 320 LAREYIYLYWSTLTITIGTTPPPVKDEEYLFVIFDFLIGLVIFATIVGVNMSNMN 379
 QY 450 ANQVFRACMDTITAYMNYSIPLVOKRVETWYETWDSQRMDESDLLKTLPTTVQLA 509
 DB 380 ATRAEFQAKIDAVHYMQFRVSKGMEAKIRWFDYLTWTKTVDEREILKJPAKLRAE 439
 QY 510 LAIDVNFISIISKVDFKCDQTMIDMLRLKSLYLPFGDFVCKGKIGKEMVIIKHGEV 569
 DB 440 IATNVHLSTLKKVRIHFDCEAGLLVELVLKLPQVFPSPGDYICRKGDIGKEMVIIKEGKL 499
 QY 570 QVLGGPDGTVLTKAGSVFGEISLLAAG--GNRSTANVAVGFANLLTLDKTLQES 626
 DB 500 AVV-ADGVQYALLSAGSCFGEISILNIGSKVGNRTANIRSLGYSDLFCLSKDLMLE 558
 QY 627 ILVHYPDSERILMKARVLLKQAKTAE---ATPPKXDLALLFPKPEETPKFXTLLGGT 683
 DB 559 AVTEYPAKVKVLEGRGAILMKGLLDENEVATSMVEVDVQELGQLETNMETLYTRFG-- 616
 QY 684 GKASLALLKLRQAQKENSEGGEKEKEDKQEN--EDKQKENEKQKENE-- 739
 DB 617 -----RL-----ABYGAQOKLKQRIITVLETRMKQN-----NEDDY 648
 QY 740 -KDKGREPEKPLDRP 754
 DB 649 LSDGMNSPELAADPE 664

RESULT 9
 US-09-842-758-73
 ; Sequence 73, Application US/09842758
 ; Publication No. US20030083244A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vernet, Corine A. M.

; APPLICANT: Fernandes, Elma R
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Boldog, Ferenc L
 ; APPLICANT: Zerhusen, Bryan D
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Majumder, Kumud
 ; APPLICANT: Tcherny, Velizar T
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Gangolli, Baha A
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Taupier, Raymond J
 ; APPLICANT: Grosse, William M
 ; APPLICANT: Edward, Szekeres S
 ; APPLICANT: Alsobrook II, John P
 ; TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-783
 ; CURRENT APPLICATION NUMBER: US/09/842,758
 ; PRIOR FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: 60/200,158
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: 60/200,613
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,780
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/201,006
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,007
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,236
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,238
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/201,186
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: 60/201,474
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/201,508
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 60/220,591
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: 60/232,678
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: 60/263,217
 ; PRIOR FILING DATE: 2001-01-22
 ; PRIOR APPLICATION NUMBER: 60/265,160
 ; PRIOR FILING DATE: 2001-01-30
 ; NUMBER OF SEQ ID NOS: 113
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 73
 ; LENGTH: 732
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 US-09-842-758-73

Query Match 19.4%; Score 820; DB 10; Length 732;
 Best Local Similarity 28.8%; Pred. No. 2.2e-54;
 Matches 222; Conservative 132; Mismatches 306; Indels 112; Gaps 21;
 QY 24 SRNEEGHSPNSQOQTAAENKGB-----EKSLTKTPTVTSEEPHNTIQ 70
 DB 32 TKRKWSGKGTQSTQCTETRRRAQTFCBSTGHTWMTKSNKGVKSSPANN---HNNHV 88
 QY 71 DKLSKSSGDLTTPQNAAEPTGTVPQK--EMDPGKGPNSQNKPPAAPVINEYA 128
 DB 89 PATIKANGKDESRFSRPSQSAADDTSSSELQRLAEMDAPQRCRGFRIVLVGVIRQWA 148
 QY 129 -----DAQJHNLVKMRQRTALYKXKLVGDLSSPEASQTAKTAPVAPPVPEKSDDKPT 181


```
Db 149 NNFREEARPSFLERFR-----GPELQVTVTQQGDKGDKGDKGT 192
QY 182 EHYRLMFKVKMELTEYLKRIKLPNSIDSYDRLYLMLLVTL--AYNNMCWFIPLR 239
Db 193 KKKPELF-----VLDPAGD-WYYRWLFVIAMPVLYNW-CLLV-AR 229
QY 240 LVFPQTADNTHYMLADIICDILYDMLFIQPLQFVRGDDIIVDSNELKHYRTSTK 299
Db 230 ACFSDLQGYFLVWLVDYFSDVVIAD-LFIRLTGFLQGLLVKOPKLRDNYIHTLQ 288
QY 300 FOLDVASIIPEDICYLFFGF-NPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTG 358
Db 289 FKLDVASIIPDILYFAVGHNPELFRNLLHFAFMFEFDRTRTSYGNIPRISNLV 348
QY 359 YLLFILHINACVYVWASNYEGIGTRWY-----DGE-----GNEYLCYVWAVRLTIIG 410
Db 349 YILVLIHWNACIYVIAISKISGFGVDVTWYVYNTPEYGYLAREYIYCLYVSTLTLTIGE 408
QY 411 LPEPOTLEIVFQNLNFFSGVVFSSLIQMRDVIGATANQNYFRACMDDTIAYMNNYS 470
Db 409 TPPPVKDEEYLFVIFDPLIGVLIFATIVGVNGSMISNNNATRAEFQAKIDAVKHYMQFRK 468
QY 471 IPKLVQKRVRTWYETWDSQRMDESLLKLTPTVQLALADVNFSLISKVDLFKCDT 530
Db 469 VSKEMEAKVIRKWFYLTWNTKKTVDREVLKPLAKRAETAINVHLSTLKKVRFQDCEA 528
QY 531 QMIYDMLLKLKSLYLPDGFVCKGGEIGKEMYYIIGHGEVQVLGGPDGTVKLVILKAGSVF 590
Db 529 GLVVLVLRQVSPGDIYCRKDGKEMYYIIEKGLAVV-ADDGVTQVALLSAGSCF 587
QY 591 GRISILLAGG---GNRRANVAVGHANLLFDKLTQELVHYVPSERILMKARVLK 647
Db 588 GEISILNTKSGOMGNRRANIRSLGYSDFCLSKDDLMEEAVTEYDPAKKVLEGRBEIM 647
QY 648 QKAKTAE---APPPKDKLALLFPPEETPKLFTLLGKTGKASLARLLKLRQEAQKKE 704
Db 648 KSGLLDENEVAASMEVDVQEKLKQLETNWTLYTRFG-----RLJ----- 687
QY 705 NSEGEERKEDNEDQKEN--EDROKEDNGKKNEDKDKGRBEPKPLDRP 754
Db 688 ---AETGAOQKLRITVLEVRKONTE---DDYLSGDMNSPEPAAAEQP 732

RESULT 10
US-10-174-333-73
; Sequence 73, Application US/10174333
; Publication NO. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Cancelli, Esha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
```

```
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10/174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 73
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
; US-10-174-333-73
```

```
Query Match 19.4%; Score 820; DB 12; Length 732;
Best Local Similarity 28.8%; Pred. No. 2.2e-54;
Matches 222; Conservative 132; Mismatches 306; Indels 112; Gaps 21;

QY 24 SRNREGSHPSNQSQTAAENKGE-----EKSLTKTPTVSEPHNIIQ 70
Db 32 TKRKWSGKGTPMSTQCTERRAQFCESTGHTWMTKSNKGVKSPANN---HNNHV 88
QY 71 DXLSKNSGSLTTPDPQNAAEPTGVPEQK--EMDPGKEGPNSPQKPPAAVINEYA 128
Db 89 PATIKANGKDESRTSRPQSAADDDTSSELQRLAEMDAPQORRGFRIRVLGVIRQWA 148
QY 129 -----DAQLNLVVRVQRQALYKKLVSGDLSSEASPTAKPTAVPVKESDDKPT 181
Db 149 NNFREEARPSFLERFR-----GPELQVTVTQQGDKGDKGDKGT 192
QY 182 EHYRLMFKVKMELTEYLKRIKLPNSIDSYDRLYLMLLVTL--AYNNMCWFIPLR 239
Db 193 KKKPELF-----VLDPAGD-WYYRWLFVIAMPVLYNW-CLLV-AR 229
QY 240 LVFPQTADNTHYMLADIICDILYDMLFIQPLQFVRGDDIIVDSNELKHYRTSTK 299
Db 230 ACFSDLQGYFLVWLVDYFSDVVIAD-LFIRLTGFLQGLLVKOPKLRDNYIHTLQ 288
QY 300 FOLDVASIIPEDICYLFFGF-NPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTG 358
Db 289 FKLDVASIIPDILYFAVGHNPELFRNLLHFAFMFEFDRTRTSYGNIPRISNLV 348
QY 359 YLLFILHINACVYVWASNYEGIGTRWY-----DGE-----GNEYLCYVWAVRLTIIG 410
Db 349 YILVLIHWNACIYVIAISKISGFGVDVTWYVYNTPEYGYLAREYIYCLYVSTLTLTIGE 408
QY 411 LPEPOTLEIVFQNLNFFSGVVFSSLIQMRDVIGATANQNYFRACMDDTIAYMNNYS 470
Db 409 TPPPVKDEEYLFVIFDPLIGVLIFATIVGVNGSMISNNNATRAEFQAKIDAVKHYMQFRK 468
QY 471 IPKLVQKRVRTWYETWDSQRMDESLLKLTPTVQLALADVNFSLISKVDLFKCDT 530
Db 469 VSKEMEAKVIRKWFYLTWNTKKTVDREVLKPLAKRAETAINVHLSTLKKVRFQDCEA 528
```



```

Db 260 FDTETRTNYPNIPRISNLVLYLVIIHWNACIYYAISKSIGFGVDTWVYFNITDPEYGY 319
QY 391 -GNEVLCRYVAVRTLIITIGLPEPQTLFETVQOLLNPFSGVFSSLIQOMRDVIGAA 449
Db 320 LAREVIYCLYNSTLTATIGTTPPVKDEEYLFVDFLGLVLIATVGNVGSIMNN 379
QY 450 ANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYETWDSQRLMDESLLKTLPTTVOLA 509
Db 380 ATRAEFOAKIDAVKHYNQFRKVSQKMEAKVIRWFDYLTWTKTVDREILKNLPKLA 439
QY 510 LAIDVNFIIISKVDLFKGCDDTQMYDMLRLKSVLYLPDGVCKKGIGKEMVIIKHGEV 569
Db 440 IAINVHLSTLKKVRIHFDCEAGLVELVLKRPQVPSFGDYICRKGDIKEMVIIKEGL 499
QY 570 QVLGPDGTQVLTWKAGSVFGEISLLAAG--GNRRTANVVAHGFANLLTLDKKTLOE 626
Db 500 AVV-ADDGVTQYALLSAGSCFGEISILNKGSKMGNRTANIRSLGYSDFCLSKODLME 558
QY 627 ILVHPDSEIRILMKARVLLKQAKTAE--ATPPKDLALLFPKBEETKFLKTLGGT 683
Db 559 AVTEYDPAKVLBERGRILMKEGLLDENEVATSMEDVQEKLGQLETNMTLYTRFG-- 616
QY 684 GKASLARLLKLRQAAQKENSEGEGEKENEDKOKEN--EDKOKENEDKOKENED-- 739
Db 617 -----RL-----ABYTGAQQLKQRTVLETKMKN-----NEDDY 648

RESULT 13
US-10-034-843-2
; Sequence 2, Application US/10034843
; Publication No. US2002011478A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; TITLE OF INVENTION: NO. US2002011478A1 Human Ion Channel Protein and Polynucleotide
; FILE REFERENCE: LEX-0291-USA
; CURRENT APPLICATION NUMBER: US/10/034,843
; CURRENT FILING DATE: 2001-12-27
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 664
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-034-843-2

Query Match 19.4%; Score 619.5; DB 13; Length 664;
Best Local Similarity 29.5%; Pred. No. 2.1e-54;
Matches 217; Conservative 129; Mismatches 285; Indels 105; Gaps 21;

QY 50 EKSLTKTPTVTSBEPHNIQDKLSKNSSDGLTNDPPQNAAPPTGTVEQK--EWDPG 107
Db 3 EKTNGVSKSPANNHHA---PPAKANGKDDHRTSRPHSAADDDTSSQLQRLADVAP 59
QY 108 KEGNPSQNKPPAAPVINEYADAOLH-----NLVRMRQRTALYKKLVGDLSSPEA 160
Db 60 QQGRSGFRIRVLVGLIREWANKNFRPEPRDPSFLERF-----GPEL 103
QY 161 SPQAKTAPVAPVKESDDKPTHEYRLWLVFKVKKMPLTEYLKRLPNSIDSTYDLRYLL 220
Db 104 QTVT--QEGGKGDKGDKGDKGKKKFFLF-----VLDPAQD-WYIC 142
QY 221 WLLVTL--AYNWCNCFPLRVPYQADNIHYWLIADIICDIILYDMLFTQPLQFV 278
Db 143 WLFVIAFVLVNW-CLLV-ARACFSDLKQGYLVWLVLDVYSDVVIAD-LFIRLTGFL 199
QY 279 RGGDIIVDSNELRKHRTSTKQLDVASIIIPFDICYLFFGCF-NPMFRANRLKYTSFFEF 337

```

```

Db 200 EQGLLVKDTKKLRNYIHTLQFLDVASIIIPDTLIYFAVDIHSPEVFRNELLHPARMEF 259
QY 338 NHLESIMDKAYIYKRVIRTTGYLLFILHINACVYVWASNYEGIGTRRWVY---DGE--- 390
Db 260 FDTETRTNYPNIPRISNLVLYLVIIHWNACIYYAISKSIGFGVDTWVYFNITDPEYGY 319
QY 391 -GNEVLCRYVAVRTLIITIGLPEPQTLFETVQOLLNPFSGVFSSLIQOMRDVIGAA 449
Db 320 LAREVIYCLYNSTLTATIGTTPPVKDEEYLFVDFLGLVLIATVGNVGSIMNN 379
QY 450 ANQNYFRACMDDTIAYMNNYSIPKLVQKRVRTWYETWDSQRLMDESLLKTLPTTVOLA 509
Db 380 ATRAEFOAKIDAVKHYNQFRKVSQKMEAKVIRWFDYLTWTKTVDREILKNLPKLA 439
QY 510 LAIDVNFIIISKVDLFKGCDDTQMYDMLRLKSVLYLPDGVCKKGIGKEMVIIKHGEV 569
Db 440 IAINVHLSTLKKVRIHFDCEAGLVELVLKRPQVPSFGDYICRKGDIKEMVIIKEGL 499
QY 570 QVLGPDGTQVLTWKAGSVFGEISLLAAG--GNRRTANVVAHGFANLLTLDKKTLOE 626
Db 500 AVV-ADDGVTQYALLSAGSCFGEISILNKGSKMGNRTANIRSLGYSDFCLSKODLME 558
QY 627 ILVHPDSEIRILMKARVLLKQAKTAE--ATPPKDLALLFPKBEETKFLKTLGGT 683
Db 559 AVTEYDPAKVLBERGRILMKEGLLDENEVATSMEDVQEKLGQLETNMTLYTRFG-- 616
QY 684 GKASLARLLKLRQAAQKENSEGEGEKENEDKOKEN--EDKOKENEDKOKENED-- 739
Db 617 -----RL-----ABYTGAQQLKQRTVLETKMKN-----NEDDY 648

RESULT 14
US-10-168-651-7
; Sequence 7, Application US/10168651
; Publication No. US20030171275A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: YANG, Junning
; APPLICANT: REDDY, Roopa
; APPLICANT: LAL, Preeti
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: AZIMZAI, Valda
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: YAO, Monique G.
; APPLICANT: GANDHI, Aneeni R.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; TITLES OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0005 PCT
; CURRENT APPLICATION NUMBER: US/10/168,651
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/178,572; 60/179,758; 60/181,625
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-21; 2000-01-28; 2000-02-02; 2000-02-10
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 17:15:34 ; Search time 10368.6 Seconds
(without alignments)
11299.126 Million cell updates/sec

Title: US-09-855-828-2
Perfect score: 2703
Sequence: 1 cattctctactttaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.to:*
11: gb.ats:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.to:*
27: em.ats:*
28: em.un:*
29: em.vi:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pln:*
35: em.htg.rod:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2667.4	98.7	4369	9	AF272900	AF272900 Homo sapi
2	2108.4	78.0	2135	9	AF228520	AF228520 Homo sapi
3	1822.8	67.4	2826	4	AF490511	AF490511 Canis fam
4	1452	53.7	4710	10	MMU243572	MMU243572 Mus muscu
5	577.4	21.4	3025	9	HUMCNQCB	LI5237 Homo sapien
6	577.4	21.4	3408	9	HUMCNQCCA	LI5236 Homo sapien
7	577.4	21.4	4033	9	HSU58837	U58837 Human CGMP-
8	577.4	21.4	4382	9	AF042498	AF042498 Homo sapi
9	575.2	21.3	4763	10	BC045114	BC045114 Mus muscu
10	572.2	21.2	3083	4	AF074012	AF074012 Bos tauru
11	572.2	21.2	3090	4	AF074013	AF074013 Bos tauru
12	572.2	21.2	3253	4	BTCNG4CGN	X94707 B.taurus mr
13	572.2	21.2	3290	4	AF074014	AF074014 Bos tauru
14	572.2	21.2	4282	4	BTRPCNGCL	X89626 B.taurus mr
15	569.6	21.1	4238	10	RNCNG41	AJ000496 Rattus no
16	568	21.0	3236	10	RNCNG43	AJ000515 Rattus no
17	568	21.0	3328	10	AF068572	AF068572 Rattus no
18	521.4	19.3	205816	9	AC013751	AC013751 Homo sapi
19	237.4	8.8	2511	3	CEU73476	U73476 caenorhabdi
20	223	8.3	3358	3	BT001439	BT001439 Drosophil
21	217.8	8.1	3099	10	BC046523	BC046523 Mus muscu
22	196.2	7.3	441	10	AF015728	AF015728 Rattus no
23	192.4	7.1	187022	9	AC090572	AC090572 Homo sapi
24	192.4	7.1	189126	2	AC021132	AC021132 Homo sapi
25	187.4	6.9	1709	3	AY060725	AY060725 Drosophil
26	181.2	6.7	2061	4	SSU85404	U85404 Sus scrofa
27	181.2	6.7	2857	9	S42457	S42457 CNGU-rod ph
28	176.8	6.5	2697	4	CFACGMP	X99914 C.familiari
29	176.8	6.5	2717	4	CFU83905	U83905 Canis famil
30	176.4	6.5	2500	9	HUMCGMP	M84741 Human CGMP-
31	175	6.5	201246	10	AL683894	AL683894 Mouse DNA
32	173.6	6.4	2682	4	BTCGMECH	X51604 B.taurus RN
33	169.8	6.3	1674	9	AF547222	AF547222 Homo sapi
34	169.8	6.3	181804	9	AC107068	AC107068 Homo sapi
35	166.8	6.2	233700	2	AC117107	AC117107 Rattus no
36	166.4	6.2	2297	10	MMU19717	U19717 Mus musculu
37	164.8	6.1	2474	10	MUSCNCG	M84742 Mus musculu
38	162.4	6.0	6312	3	AF091302	AF091302 Limulus p
39	161.4	6.0	58409	10	AL772281	AL772281 Mouse DNA
40	155.6	5.8	2612	5	GGRODCNG	X89599 G.gallus mr
41	152	5.6	2052	10	RNU48803	U48803 Rattus norv
42	150.6	5.6	200535	10	AL671880	AL671880 Mouse DNA
43	150.6	5.6	222930	2	AC099698	AC099698 Mus muscu
44	150.2	5.6	181805	2	AC114445	AC114445 Rattus no
45	150.2	5.6	190000	2	AC007704	AC007704 Homo sapi

ALIGNMENTS

RESULT 1	AF272900	4369 bp	mrna	linear	PRI 29-AUG-2000
LOCUS	AF272900	Homo sapiens cone photoreceptor cyclic nucleotide-gated channel			
DEFINITION	beta subunit (CNGB3) mRNA, complete cds.				
ACCESSION	AF272900				
VERSION	AF272900.1	GI:9247065			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 4369) Kohl,S., Baumann,B., Broghammer,M., Jagle,H., Sieving,P., Kellner,U., Spegal,R., Anastasi,M., Zrenner,E., Sharpe,L.T. and				

Wissinger, B.
Mutations in the CNGB3 gene encoding the beta-subunit of the cone
photoreceptor cGMP-gated channel are responsible for achromatopsia
(ACHM3) linked to chromosome 8q21
Hum. Mol. Genet. 9 (14), 2107-2116 (2000)
2044632
10958649
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
SUBMITTED (30-MAY-2000) University Eye Hospital, Molecular Genetics
Laboratory, Auf der Morgenstelle 15, Tuebingen D-72076, Germany
Location/Qualifiers
1. .4369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1. .4369
/gene="CNGB3"
47. .2476
/gene="CNGB3"
/codon_start=1
/product="cone photoreceptor cyclic nucleotide-gated
channel beta subunit"
/protein_id="BAF6274.1"
/db_xref="GI:9247066"
/translation="MFSLTKVKNKPIGENNENESQSRNBEHSPNSQOQTAE
ENKGEKSLKTSPTVSEEPHTNIQDKLSKSSGDLTTPDPONAAPTGTVPKQ
EMDPCKEGSPQKPPAAPVINEYADAQLNLRMRQRTALYKKLVGDLSSPA
SPQAKPTAPVPVKESDDKPTHEVYRLMFKVKOMPLTEYLKIKLPSNDSVTDRLY
LLMLLVLAANNMCPRLPLSVFYOTADNIHWLADIIICDILVDMFLTPRLQ
FVRGDIIVDSNELKXHYRSTKEQLVASIIPEDICYLFEFNPFRANRMLKITSF
FEFNHLSIMDKAIIIRKTYGTLFLILHINACVYIWNASNYEGIGTTTWDGEGN
EYLKYVWAVRLITIGLPEPOTFEIIVFOLLNFFSGVVFVSLIGQMRDVIKAATA
NONFRACMDTIAMNYSIPKLVQRVETWYTWDSQRLDSEDLKLTLPVVK
ALADVNFISIKVLDLFGCDQIMYDMRLRLKSLVLPDGFVCKEIGKEMVIKH
GEVVLVGPDRILKVLKAGSVFGEISLLAAGGNRRTANVVAHGFANLLTDKTL
QELIVHPDSRILMKVRLVKOKAKTEATPPKDLALLFPKPEPPLKFLTLGG
TGKSLARLLKLEQAKKENSEGSEBEKEDKQENEDKQENEDKQENEDK
DKGREPEKPLDRECFASPIAVIEEPHVSRRVRLPRGTSRQSLIISMAPSABGSEV
LTIEVKEKAKQ"

Query Match 98.7%; Score 2667.4; DB 9; Length 4369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2668; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 GGCACAGTCATAAATACAGAGGGTTTTCAGAACCACTCAGAGAAGATGTTAAATCGCT 76
DB 1 GGCACAGTCATAAATACAGAGGGTTTTCAGAACCACTCAGAGAAGATGTTAAATCGCT 60

QY 77 GACAAAAGTCAACAGGTGAAGCTTATAGAGAGAACAAATGAGAACAAAGTCTTCG 136
DB 61 GACAAAAGTCAACAGGTGAAGCTTATAGAGAGAACAAATGAGAACAAAGTCTTCG 120

QY 137 TCGGAATGAAGAAGCTCTCACCAAGTAATCAGTCTCAGCAAAACACACAGGAAGA 196
DB 121 TCGGAATGAAGAAGCTCTCACCAAGTAATCAGTCTCAGCAAAACACACAGGAAGA 180

QY 197 AAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCACTCCAGTCCAGTCTCAAGAGCC 256
DB 181 AAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCACTCCAGTCCAGTCTCAAGAGCC 240

QY 257 ACACCAACATACAGACAAATCTCTCCAGAAAAATTCCTCTGGAGATCTGACCAACAAA 316
DB 241 ACACCAACATACAGACAAATCTCTCCAGAAAAATTCCTCTGGAGATCTGACCAACAAA 300

QY 317 CCCTGACCTCAAAATCAGACAGAACCAACTGAAACAGTCCGACAGAGAGAAATGGA 376
DB 301 CCCTGACCTCAAAATCAGACAGAACCAACTGAAACAGTCCGACAGAGAGAAATGGA 360

QY 377 CCCCGGAAAGAGGTCCAAACAGCCCAACAAACCAACCCGCTTCGAGCTCCTGTTATAAA 436

DB 361 CCCCGGAAAGAGGTCCAAACAGCCCAACAAACAAACCCGCTTCGAGCTCCTGTTATAA 420
QY 437 TGAGTATGCCGATGCCAGCTACAAACCTGGTGAAGAAATGCGTCAAGAACAGCCCT 496
DB 421 TGAGTATGCCGATGCCAGCTACAAACCTGGTGAAGAAATGCGTCAAGAACAGCCCT 480
QY 497 CTACAGAAAAAAGTTCGTAGAGGAGATCTCTCTCACCAGGAGCCAGCCCAAACTGC 556
DB 481 CTACAGAAAAAAGTTCGTAGAGGAGATCTCTCTCACCAGGAGCCAGCCCAAACTGC 540
QY 557 AAAGCCCAAGGCTGTACCAACAGTAAAGAAAGCGATGATAGCCCAAGACATTA 616
DB 541 AAAGCCCAAGGCTGTACCAACAGTAAAGAAAGCGATGATAGCCCAAGACATTA 600
QY 617 CAGGCTGTGTGGTTCARAGTCAAAAGATGCTTTTACAGAGTACTTAAAGCGAATAA 676
DB 601 CAGGCTGTGTGGTTCARAGTCAAAAGATGCTTTTACAGAGTACTTAAAGCGAATAA 660
QY 677 ACTTCCAAAACAGCATAGATTACACAGATCGACTCTATCTCTCTGTGGCTCTTCTTGT 736
DB 661 ACTTCCAAAACAGCATAGATTACACAGATCGACTCTATCTCTCTGTGGCTCTTCTTGT 720
QY 737 CACTCTTGCTATATAGTGAATCTGCTGTTTATACACATCGCCCTCGTCTCCCATATCA 796
DB 721 CACTCTTGCTATATAGTGAATCTGCTGTTTATACACATCGCCCTCGTCTCCCATATCA 780
QY 797 AACCGCAGACAAACATACACTACTGGCTTATTCGGACATCATATGATATCATCTACT 856
DB 781 AACCGCAGACAAACATACACTACTGGCTTATTCGGACATCATATGATATCATCTACT 840
QY 857 TTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAGAGAGGAGACATAATAGT 916
DB 841 TTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAGAGAGGAGACATAATAGT 900
QY 917 GGAATCAATGAGCTAAGGAAACACTACAGGACTTCTACAAATTTCAAGTTGGATGTCG 976
DB 901 GGAATCAATGAGCTAAGGAAACACTACAGGACTTCTACAAATTTCAAGTTGGATGTCG 960
QY 977 ATCAATATACCAATTTGATTTGCTACTCTCTCTTTCGGTTAATCAATGTTTAGAGC 1036
DB 961 ATCAATATACCAATTTGATTTGCTACTCTCTCTTTCGGTTAATCAATGTTTAGAGC 1020
QY 1037 AAATAGGATGTAAGAGTACACTTCAATTTTGAATTTAATCATCATCTAGATCTATAAT 1096
DB 1021 AAATAGGATGTAAGAGTACACTTCAATTTTGAATTTAATCATCATCTAGATCTATAAT 1080
QY 1097 GCACAAAGCATATATCTACAGAGTTTATTCGAACAACTGGATACTTGTGTTTATCTGCA 1156
DB 1081 GCACAAAGCATATATCTACAGAGTTTATTCGAACAACTGGATACTTGTGTTTATCTGCA 1140
QY 1157 CATTAATGCTGTGTTTATTTACTGGCTTCAAACTAAGAGAAATTCGCACTACTAGATG 1216
DB 1141 CATTAATGCTGTGTTTATTTACTGGCTTCAAACTAAGAGAAATTCGCACTACTAGATG 1200
QY 1217 GGTGTATGATGGGAGGAAACGAGATCTCAGAGATGTTTATTTGGGAGTTTCAACTTT 1276
DB 1201 GGTGTATGATGGGAGGAAACGAGATCTCAGAGATGTTTATTTGGGAGTTTCAACTTT 1260
QY 1277 AATTAACCATGCTGGCTTCCAGAACCAAACTTTTATTTGAAATTTGTTTTCACCTTT 1336
DB 1261 AATTAACCATGCTGGCTTCCAGAACCAAACTTTTATTTGAAATTTGTTTTCACCTTT 1320
QY 1337 GAATTTTTTTCTGGAGTTTTTGTCTCCAGTTTAAATTTGGTCAGATGAGAGATGAT 1396
DB 1321 GAATTTTTTTCTGGAGTTTTTGTCTCCAGTTTAAATTTGGTCAGATGAGAGATGAT 1380
QY 1397 TGGAGCAGTACAGCCCAATCAGAACTACTTCCGCGCTCGATGATGATGACACCATGCTTA 1456
DB 1381 TGGAGCAGTACAGCCCAATCAGAACTACTTCCGCGCTCGATGATGATGACACCATGCTTA 1440
QY 1457 CATGAACAAATTTACTTCCATTTCTAACTTTGTCGAAAGCGAGTTTCGGACTTGGATGATA 1516
DB 1441 CATGAACAAATTTACTTCCATTTCTAACTTTGTCGAAAGCGAGTTTCGGACTTGGATGATA 1500

QY	1517	TACATGGAGCTCTCAAGAATGCTACATGAGTCTGATTGTTCCTTAAGACCCCTACCACACTAC	1576
DB	1501	TACATGGAGCTCTCAAGAANAAGCTAGATGAGTCTGAATTTGGCTTAAGACCCCTACCACACTAC	1560
QY	1577	GGTCCAGTTAGCCCTCGCCATTGATGTGAACCTTCAGCATCATCAGCAAAGTGACATTGTT	1636
DB	1561	GGTCCAGTTAGCCCTCGCCATTGATGTGAACCTTCAGCATCATCAGCAAAGTGACATTGTT	1620
QY	1637	CAAGGGTTGTATACACAGATGATTTATGCATGTTTGCCTAAGATTGAAATCCGGTCTCTTA	1696
DB	1621	CAAGGGTTGTATACACAGATGATTTATGCATGTTTGCCTAAGATTGAAATCCGGTCTCTTA	1680
QY	1697	TTTTGCCCTGGTGCACTTTTCTCGCAAAAAGGAGAAAAATTGGCAAGAAATGTATATCATCAA	1756
DB	1681	TTTTGCCCTGGTGCACTTTTCTCGCAAAAAGGAGAAAAATTGGCAAGAAATGTATATCATCAA	1740
QY	1757	GCAATGGAGAAGTCCAAGTTCTTGGAGCCCTGATGTTACTATAAGTTTCTGGTTACTCTGAA	1816
DB	1741	GCAATGGAGAAGTCCAAGTTCTTGGAGCCCTGATGTTACTATAAGTTTCTGGTTACTCTGAA	1800
QY	1817	AGCTGGGTGGTGTGTTGGAGAAATCAGCCCTTCAGCAGCAGGAGGAGAAACCGTCGAAC	1876
DB	1801	AGCTGGGTGGTGTGTTGGAGAAATCAGCCCTTCAGCAGCAGGAGGAGAAACCGTCGAAC	1860
QY	1877	TGCCAATGTGGTGCCCAACGGTTTGCCAAATCTTTTHAATCTTAGAChAAAGAACCTTCCA	1936
DB	1861	TGCCAATGTGGTGCCCAACGGTTTGCCAAATCTTTTHAATCTTAGAChAAAGAACCTTCCA	1920
QY	1937	AGAAATTTCTAGTGCAATTATCCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGCT	1996
DB	1921	AGAAATTTCTAGTGCAATTATCCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGCT	1980
QY	1997	TTTTAAAGCAGAGGCTAAGACCGCAGAAAGCAACCCCTCCAAGAAAGATCTTGCCCTCTCT	2056
DB	1981	TTTTAAAGCAGAGGCTAAGACCGCAGAAAGCAACCCCTCCAAGAAAGATCTTGCCCTCTCT	2040
QY	2057	CTTCCCACCGAAGAGACGACCCAACTGTTTAAACTCTCTCTAGAGGSCACAGAAA	2116
DB	2041	CTTCCCACCGAAGAGACGACCCAACTGTTTAAACTCTCTCTAGAGGSCACAGAAA	2100
QY	2117	AGCAAGTCTTCCAAGACTACTCAAATTTGAACGAGACAAGCAGCTCAGAAAGAAAGAAA	2176
DB	2101	AGCAAGTCTTCCAAGACTACTCAAATTTGAACGAGACAAGCAGCTCAGAAAGAAAGAAA	2160
QY	2177	TTCTGAAGGAGGAGAGGAAGGAAGAANAATGAAGATAAACAANAAGAAATGAAGA	2236
DB	2161	TTCTGAAGGAGGAGAGGAAGGAAGAANAATGAAGATAAACAANAAGAAATGAAGA	2220
QY	2237	TAAACAAAAGAAAATGAAGATAAAGGAAAAGAAAATGAAGATAAAGAAAGAGAGA	2296
DB	2221	TAAACAAAAGAAAATGNAGATAAAGGAAAAGAAAATGAAGATAAAGAAAGAGAGA	2280
QY	2297	GCCAGAAGAGAGCCACTGGGACAGACTGAATGTACAGCAAGTCTCTATTGCAGTGGAGGA	2356
DB	2281	GCCAGAAGAGAGCCACTGGGACAGACTGAATGTACAGCAAGTCTCTATTGCAGTGGAGGA	2340
QY	2357	AGAACCCCACTCAGTTAGAAGACAGTTTACCAGAGGGAGTCTCGTCAATCACTCAT	2416
DB	2341	AGAACCCCACTCAGTTAGAAGACAGTTTACCAGAGGGAGTCTCGTCAATCACTCAT	2400
QY	2417	TATCAGCATGGCTCTCTCTGTCGGGCGGAGAGAGGTTCTTACTATTGAAGTCAAAGA	2476
DB	2401	TATCAGCATGGCTCTCTCTGTCGGGCGGAGAGAGGTTCTTACTATTGAAGTCAAAGA	2460
QY	2477	AAAGGCTAAGCAATAAATGTTTGATTATCTTTAGATGTGATATAGCTAGTTCCCCAAAGTG	2536
DB	2461	AAAGGCTAAGCAATAAATGTTTGATTATCTTTAGATGTGATATAGCTAGTTCCCCAAAGTG	2520
QY	2537	ATTGTACCTAGGATTGTAACTTTAAATTAACGAGGGGAAACGACATGCTGGGACCTTTGAG	2596
DB	2521	ATTGTACCTAGGATTGTAACTTTAAATTAACGAGGGGAAACGACATGCTGGGACCTTTGAG	2580

2597 AAACGAAAGCAAAATCCCTAGTCTTAGTTCTCAGGAATTATCTCAGAGTGATGTTCATGC 2655
 Db |-----|
 2581 AAACGAAAGCAAAATCCCTAGTCTTAGTTCTCAGGAATTATCTCAGAGTGATGTTCATGC 2640
 QY |-----|
 2657 AGTCGTAATAAAGAGATTATTAAGAACA 2685
 Db |-----|
 2641 AGTGGTAATAAAGAGATTATTAAGAACA 2669
 QY |-----|

```

RESULT 2
AF228520      2135 bp mRNA linear PRI 30-JUN-2000
LOCUS Homo sapiens cone photoreceptor cGMP-gated cation channel
DEFINITION beta-subunit (CNGB3) mRNA, complete cds.
ACCESSION AF228520
VERSION AF228520.1 GI:8843947
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2135)
AUTHORS Sundin,O.H., Yang,J.M., Li,Y., Zhu,D., Hurd,J.N., Mitchell,T.N.,
Silva,E.D. and Maumenee,I.H.
TITLE Genetic basis of total colourblindness among the Pingelapese
islanders
JOURNAL Nat. Genet. 25 (3), 289-293 (2000)
MEDLINE 20347712
PUBMED 10888875
REFERENCE 2 (bases 1 to 2135)
AUTHORS Sundin,O.H., Yang,J.-M., Li,Y., Zhu,D., Silva,E.D. and
Maumenee,I.H.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2000) Ophthalmology, Johns Hopkins School of
Medicine, 600 North Wolfe Street, Baltimore, MD 21287, USA
FEATURES
source
1..2135
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8q21-q22"
/tissue_type="retina"
1..2135
/gene="CNGB3"
244..2076
/gene="CNGB3"
/note="membrane channel; CNGA3; core channel domain"
/codon_start=1
/product="cone photoreceptor cGMP-gated cation channel
beta-subunit"
/protein_id="AAF80179.1"
/db_xref="GI:8843948"
/t_xref="translation=WP1TEYLKRIKLPSIDSYTDRLVLLWLLVTLAYNWNCCFIPR
RLVPYPQTADNIHWLADIICDILLYLDMLFIQPLQFVVGDDIIVDSNELRKHYRV
STKFQDLVASIIIPDICVLFPFGFMFRANMLKYTFEPFNHLESIMDKAYIVRVV
RTTGYYLFILHNACVYWASNYEGITRWVIDGEYELCYRIQAWRTLTITIGGLL
EPOTLRFIVFOLLNPFVGSVFSSLIQMQRDVI GAATANQNYFRACMDDTLAYMNNY
IKPLVQRVRFTWRYETWSDSQMSDESILLPTPTVOLALAIDVNFSIISKVDLPFKG
IOWYLMWLKRSLVLPFGVCKKGIGKEMVI IKHGEVQLGGPDGTKVLTILK
GSMVLAAGGNRRNTAVVAGFANLLTLDKXTLOBILVHPDSEIRILMKKARVILKQ
AKTAEATPPRKDLLALPPKEETPKIKTLLGGTGKSLARLLKLRQQAQKKNSI
GGEEGENEDKNEDKQKENEDKQENEDKQREPEEKPLDRPCTASPIAVE
EPHSVRRVTLPFRGTSROSLLISMAPSGEGEVLTIEVKAKQ"

```

Query Match	78.0%;	Score 2108.4;	DB 9;	Length 2135;
Best Local Similarity	99.3%;	Pred. No. 0;		
Matches 2134;	Conservative	0;	Mismatches 1;	Indels 15; Gaps 1;

QY 402 CCACAAAACAAACCGCTGAGTCTCTTTTAAATGATGATGCCGATGCCAGTACAC 461
 Db 1 CCACAAAACAAACCGCTGAGTCTCTTTTAAATGATGATGCCGATGCCAGTACAC 60

QY 462 AACCTGGTGAAGAATGCGTCAAGAAACAGCCCTCTACAGAAAGAGTTGGTAGAGGA 521
 Db 61 AACCTGGTGAAGAATGCGTCAAGAAACAGCCCTCTACAGAAAGAGTTGGTAGAGGA 120
 QY 522 GATCTCTCTCACCGAGCGAGCCCAAACTGCAAGAGCCACGCGTGTACCAAGCA 581
 Db 121 GATCTCTCTCACCGAGCGAGCCCAAACTGCAAGAGCCACGCGTGTACCAAGCA 180
 QY 582 AAAGAAGCGATGATGAAGCAACAGAAATTAATCTACAGCGTGTGTGGTTCAAGTCAA 641
 Db 181 AAAGAAGCGATGATGAAGCAACAGAAATTAATCTACAGCGTGTGTGGTTCAAGTCAA 240
 QY 642 AAGATGCCCTTTAAGAGAGTACTTAAGGGAATTAACCTTCAAGAGATAGATCATAC 701
 Db 241 AAGATGCCCTTTAAGAGAGTACTTAAGGGAATTAACCTTCAAGAGATAGATCATAC 300
 QY 702 ACAGATCGACTCTATCTCTCTGGTCTCTTGTGCTGCTCTGCTATTAAGTCAAGTGC 761
 Db 301 ACAGATCGACTCTATCTCTCTGGTCTCTTGTGCTGCTCTGCTATTAAGTCAAGTGC 360
 QY 762 TGGTTTATACCACTCGGCTCTCTTCCATATCAAAACCGAGACAACATCACTACTGG 821
 Db 361 TGGTTTATACCACTCGGCTCTCTTCCATATCAAAACCGAGACAACATCACTACTGG 420
 QY 822 CTATTGGGACATCATATGATATCATCTACCTTTATGATATGATATGATATGATATG 881
 Db 421 CTATTGGGACATCATATGATATCATCTACCTTTATGATATGATATGATATGATATG 480
 QY 882 AGACTCCAGTTTGAAGAGAGGAGACATAATAGTGGATTCAAATGAGCTAAGGAACAC 941
 Db 481 AGACTCCAGTTTGAAGAGAGGAGACATAATAGTGGATTCAAATGAGCTAAGGAACAC 540
 QY 942 TACAGGACTTCTACAAATTTTCAGTTGATGATGATGATGATGATGATGATGATGAT 1001
 Db 541 TACAGGACTTCTACAAATTTTCAGTTGATGATGATGATGATGATGATGATGATGAT 600
 QY 1002 TACCTCTCTCTTGGGTTTAAATCCAAATGTTAGCAAAATAGATGTTAAAGTACACTTCA 1061
 Db 601 TACCTCTCTCTTGGGTTTAAATCCAAATGTTAGCAAAATAGATGTTAAAGTACACTTCA 660
 QY 1062 TTTTGTGAATTAATCATCTAGAGTCTAATATGAGCAAGCATATATCTACAGATT 1121
 Db 661 TTTTGTGAATTAATCATCTAGAGTCTAATATGAGCAAGCATATATCTACAGATT 720
 QY 1122 ATTCGAACAACTGGATCTCTGTTTATCTGACATTAATGCTGCTGTTTATCTG 1181
 Db 721 ATTCGAACAACTGGATCTCTGTTTATCTGACATTAATGCTGCTGTTTATCTG 780
 QY 1182 GCTTCAAACTAAGGAATTTGGCACTACTAGATGGGTGTATGATGGGAGGAACGAG 1241
 Db 781 GCTTCAAACTAAGGAATTTGGCACTACTAGATGGGTGTATGATGGGAGGAACGAG 840
 QY 1242 TATCTGAGATCTATTATTTGGGAGTTCGAACTTAAATACCATTTGGTGGCTTCCAGAA 1301
 Db 841 TATCTGAGATCTATTATTTGGGAGTTCGAACTTAAATACCATTTGGTGGCTTCCAGAA 900
 QY 1302 CCACAACTTTATTTGAATTTGTTTTCAACTCTTGAATTTTTTTCTGGAGTTTGTG 1361
 Db 901 CCACAACTTTATTTGAATTTGTTTTCAACTCTTGAATTTTTTTCTGGAGTTTGTG 960
 QY 1362 TTCTCCAGTTTAAATTTGGTCAGATGAGATGTGATTTGGAGCAGCTACAGCAATCAGAAC 1421
 Db 961 TTCTCCAGTTTAAATTTGGTCAGATGAGATGTGATTTGGAGCAGCTACAGCAATCAGAAC 1020
 QY 1422 TACTTCGCGCTCGATGGATGACCACTTGCCTTACATGAACAAATTAATCTCCATTCCTAAA 1481
 Db 1021 TACTTCGCGCTCGATGGATGACCACTTGCCTTACATGAACAAATTAATCTCCATTCCTAAA 1080
 QY 1482 CTCTGCAAAAGCGAGTTCGAGTTGGTATGAATATACATGGGACTCTCAAGAAATGCTA 1541
 Db 1081 CTCTGCAAAAGCGAGTTCGAGTTGGTATGAATATACATGGGACTCTCAAGAAATGCTA 1140

QY 1542 GATGAGTCTGATTTGCTTAAGACCCCTACCACTACCGTCCAGTTAGCCCTCGCCATTGAT 1601
 Db 1141 GATGAGTCTGATTTGCTTAAGACCCCTACCACTACCGTCCAGTTAGCCCTCGCCATTGAT 1200
 QY 1602 GTCAATCTCAGCATCATCAGCAAGTCGACTTGTTCAGGGTTGTGATACACAGATGATT 1661
 Db 1201 GTCAATCTCAGCATCATCAGCAAGTCGACTTGTTCAGGGTTGTGATACACAGATGATT 1260
 QY 1662 TATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTTCCCTGGTGCATTTCTCTGCAA 1721
 Db 1261 TATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTTCCCTGGTGCATTTCTCTGCAA 1320
 QY 1722 AAGGGAATTTGGCAAGGAAATGTATATCATCAAGCATGAGAGAGTCCAAATTTCTTGA 1781
 Db 1321 AAGGGAATTTGGCAAGGAAATGTATATCATCAAGCATGAGAGAGTCCAAATTTCTTGA 1380
 QY 1782 GGCCTTGATGGTACTAATAAGTTCTGTGTTACTCTGAAGCTGGTCCGTTGTTGGAGAAATC 1841
 Db 1381 GGCCTTGATGGTACTAATAAGTTCTGTGTTACTCTGAAGCTGGTCCGTTGTTGGAGAAATC 1427
 QY 1842 AGCCTTCTAGCAGCAGGAGGAGGAAACCGTCCAACTGCAATGTGGTGGCCCAACGGTTT 1901
 Db 1428 --CCTTCTAGCAGCAGGAGGAGGAAACCGTCCAACTGCAATGTGGTGGCCCAACGGTTT 1485
 QY 1902 GCCAATCTTTTAACTCTAGACAAAGACCCCTCCAGAAATTTCTAGTGCATTTATCCAGAT 1961
 Db 1486 GCCAATCTTTTAACTCTAGACAAAGACCCCTCCAGAAATTTCTAGTGCATTTATCCAGAT 1545
 QY 1962 TCTGAAAGGATCCTCATGAAAGAAAGCAGAGTGCCTTTTAAAGCAGAGGCTAAGACCCGA 2021
 Db 1546 TCTGAAAGGATCCTCATGAAAGAAAGCAGAGTGCCTTTTAAAGCAGAGGCTAAGACCCGA 1605
 QY 2022 GAAGCAACCCCTCCAAAGAAAGATCTTGGCTCTCTTCCCAACCCGAAAGAGAGACACC 2081
 Db 1606 GAAGCAACCCCTCCAAAGAAAGATCTTGGCTCTCTTCCCAACCCGAAAGAGAGACACC 1665
 QY 2082 AAATCTTTTAAACTCTCTAGGAGGACAGAGAAAGCAAGTCTTTCGAAGACTACTCAA 2141
 Db 1666 AAATCTTTTAAACTCTCTAGGAGGACAGAGAAAGCAAGTCTTTCGAAGACTACTCAA 1725
 QY 2142 TTGAAGCGAGAGCAAGCTCAGAGAAAGAAATTTCTGAAGGAGGAGAGAGAGAGGA 2201
 Db 1726 TTGAAGCGAGAGCAAGCTCAGAGAAAGAAATTTCTGAAGGAGGAGAGAGAGAGGA 1785
 QY 2202 AAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAA 2261
 Db 1786 AAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAA 1845
 QY 2262 GGAAAGAAATGAAGATAAAGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2321
 Db 1846 GGAAAGAAATGAAGATAAAGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1905
 QY 2322 CCTGATGTACAGCAAGTCTTATTTGCACTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 2381
 Db 1906 CCTGATGTACAGCAAGTCTTATTTGCACTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1965
 QY 2382 GTTTTACCCAGAGGAGTCTCTGCTCAATCACTTATCAGCATGGCTCTCTTCTGCTGAG 2441
 Db 1966 GTTTTACCCAGAGGAGTCTCTGCTCAATCACTTATCAGCATGGCTCTCTTCTGCTGAG 2025
 QY 2442 GCGGAGAGAGGTTCTTACTATTGAAGTCAAGAAAGGCTAAGCATAAATGTTGAT 2501
 Db 2026 GCGGAGAGAGGTTCTTACTATTGAAGTCAAGAAAGGCTAAGCATAAATGTTGAT 2085
 QY 2502 TATCTTTAGATGTGATATAGCTAGTTCCCAAGTGAATTTGACCTAGGATT 2551
 Db 2086 TATCTTTAGATGTGATATAGCTAGTTCCCAAGTGAATTTGACCTAGGATT 2135

RESULT 3
 AF490511
 LOCUS
 DEFINITION

Canis familiaris cyclic nucleotide gated channel beta subunit
 AF490511 mRNA linear MAM 31-JUL-2002

```
(CNGB3) mRNA, complete cds.
ACCESSION AF490511
VERSION AF490511.1 GI:22023792
KEYWORDS
SOURCE
ORGANISM Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 2826)
AUTHORS Sidjanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M.,
Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.
TITLE Canine CNGB3 mutations establish cone degeneration as orthologous
to the human achromatopsia locus ACHM3
JOURNAL Hum. Mol. Genet. 11 (16), 1823-1833 (2002)
PUBMED 12140185
REFERENCE 2 (bases 1 to 2826)
AUTHORS Sidjanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M.,
Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2002) Baker Institute, Cornell University,
Hungerford Hill Rd., Ithaca, NY 14853, USA
FEATURES
source
1..2826
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
1..2826
/gene="CNGB3"
25..2373
/gene="CNGB3"
/codon_start=1
/product="cyclic nucleotide gated channel beta subunit"
/protein_id="AAM89224.1"
/db_xref="GI:22023793"
/translation="MFKSLTIKGNKVKPRENDENKODPPSPNOPOOSTROGKNSEN
KSLQTKMPTVFESHAQMOKISEKNSLDLTPNPHCHPTSEKAMSEQKEMETGK
EGLVSPKSPGLVPIVEYADOLNLRMRORTWLYKKLAEGDISSEPEASPOQAK
PTAVPSQESNMLKREHYVHILCFKQKMLTEYLKRFELPGSIDSYDRLVLLWL
LVLIAYNNWCHLLPLRLVFPYQPDNTHYFIDITCDIILYCDMLLIOPRLOPIKGG
DIWDSNELLKRRSRTQFDVWASVNPFDVYLPFGFVFNFRNKLKITSFFENH
HLESIMDKAYIYVIRTTGYLLTHINACIYIYWDYIGIGSTRWYNGEBGKYLRC
YYWAVRLTIIGLPEPQTSFIVQLNFPFSGVFPFSSLIQGMQDVI GAATANQNF
RISMDHTISYNTYTSIPKQNVNRVRYEYTWDSQRLDESLLCTLPVTMLALVTD
NLSIIISKVLFGKCDOMIYDMLRLKSVLPGLPGPKKGIGKEMYIKOGEVQV
LGSGDGAQVLTKAGAVFGEISILLAGRGNNRTANVIAHGFANILTLKDKTLOEILV
HYDPSKLLMKKASVLLKKAPATETPPKGLAFLFPPKQETPKFKALLSGTGKAG
LTRLKKRQSTQKTSENSEGGKKREYEDKREPSFKILDSSECRANCIITAEEMP
QSIRRAALPRGTTTQSLIISWAPSAEAGEEVLITIEVKBKAKQ"
ORIGIN
Query Match 67.4%; Score 1822.8; DB 4; Length 2826;
Best Local Similarity 83.1%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 347; Indels 100; Gaps 6;
39 GTTTTCAGAACCCCTCAGAGAAGATGTTTAAATCGCTGAC---AAAAGTCACAAGGTG 95
Db 1 GTTTTCAGAACCCCTCAGAGAAGATGTTTAAATCACTGACAAATAAAATCCAAAGGTG 60
96 AAGCCTATAGAGAGACAAATGAGATGACAAAGTTCTCGTCGANTGAGAGGCTCT 155
Db 61 AAGCCTAGAGAGAGATGATGAGAAATACAAAGATCCTGAT----- 102
156 CACCCAAAGTATCATGCTCTCAGCAAAACCACAGCAGAGAGAAACAAAGGTGAAGAAA 215
Db 103 ---CCAAAGCATCAGCCTCAGCAATCTACAAGCAGGAGAGAAACAAAGTGAATAAA 159
216 TCTCTCAAAACCAAGTCACTCAGTCAAGTCTGAGAGAGCCACACCAACATCAAGAC 275
Db 160 TCTCTCAAAACCAAGTCACTCAGTCAAGTCTGAGAGATCAATGCAAAATGCAAGAT 219
276 AAACCTCCCAAGAAAATTCCTCTGGAGATCTGACCAACAAACCCCTGACCCCTCAAAATGCA 335
Db 220 AAATCTCCGAGAAAATTCCTCAGAGACCTGACGACAAATCCCAACCATCAACATCCA 279
```


Query Match				53.7%; Score 1452; DB 10; Length 4710;			
Best Local Similarity				75.4%; Pred. No. 9.4e-269;			
Matches 1976; Conservative				0; Mismatches 555; Indels 91; Gaps 10;			
Qy	19	CACAGTCAATAACAGAGGGTTTTCAGAACCCCTCAGAGAGAGATGTTTAAATPCGTGA	78	Db	1030	GAGCAATCGGATATTAAGTATACCTTCTCTTTGAGTTTAAACCATCACCTGGAGTCTA	1089
Db	40	CAGGGTCATATAATCGGAGGTCTTTCAGACCTGCTCAGAGAGAGATGTTAAATCACTGA	99	Qy	1093	TAATGGACAAGACATATATCTACAGAGTTATTCGAAACAACTGGATACCTTCTGTTTATTC	1152
Qy	79	C---AAAAGTCAACAGGTGAGGCTTATAGAGAGACAAATGAGATGAACAAAGTTCTC	135	Db	1090	TAATGGACAAGACATATATCTACAGAGTATCGGAACTATCGGAACTATGCTGTTCTCC	1149
Db	100	CAGTAAATTCACAAAGTGAATCCCATGGAGGGAGATGGAGAGAACTCT-----	153	Qy	1153	TCACATTAATCCCTGTGTGTTTATTAATGCGGCTTCAAACTATGAAGGAATGGCAGTACTA	1212
Qy	136	GTCCGAATGAAGAGGCTCTCACCAAGTAACTAGTCTCAGCAAAACCACAGCAGGAAG	195	Db	1150	TGCACTTAACGCTGTGTTTATTAATGCGGCTTCAAGACTATGAAGGAATGGCTCACTA	1209
Db	154	-----GCCCAACCTGAGCAGTCTTCTCAGCCAAACCATAGCAGCGGAG	198	Qy	1213	GATGGGTATCATGCGGGAAGGAAAACGAGTATCTCAGATGTTTATTAATGGGAGTTCGAA	1272
Qy	196	AAAACAAAGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCAGTCACTCTGAGAGC	255	Db	1210	AATGGGTCTATAATGGTGAAGGCAACAAGTATCTCGATGCTTTTATTTGGGAGTTCGAA	1269
Db	199	ACAAACCAAGTGAAGAAAGAACCTCTGAGGAGCAGG---ACACCAATCACAATTTGAAGA	255	Qy	1273	CCTTAATTAACATTTGGTGGCCTTCCAGAACCAAACTTTATTTGAAATGTTTTTTCAC	1332
Qy	256	CACACACCAATCAAGACAAACTCTCCAAGAAATAATCTCTGGAGATCTGACCACAA	315	Db	1270	CITTAATTAATCTCGGGGCTTCCAGAGCCACAGACTCATTTGAAATGTTTTTTCAT	1329
Db	256	CACACAGGAA---AGAAGACACAGCAGTGGGGAATACTCTCAGAGATTTCACCCCAA	312	Qy	1333	CTTGAATTTTTTCTCGAGTTTTTGTGTTCTCCAGTTTAAATTTGCTCAGATGAGAGATG	1392
Qy	316	ACCTGACCTTCAAAATGACAGAGAAACAACTGGAACAGTGCAGAGCAGAGAAATGG	375	Db	1330	CTTGAATTTTTTCTCGGGTTTTTGTGTTCTCCAGCTTAATTTGGTCAGATGCGTGATG	1389
Db	313	ATCTGTACCTTGAATTCGAGCAGAACTCACCAAGACAAATGGCAGAGATGGAGAAACTA	372	Qy	1393	TGATTTGAGCAGCTACAGCCAAATCAGAACTACTTCGGGCCCTGCAATGGATGACACATG	1452
Qy	376	ACCCGGGAAGAGAGTCCAAACAGCCCAACAAACCAACCGCTCGACGCTCTGTTATAA	435	Db	1390	TGATTTGGGCGACCAACAGCCAAATCAGAACTACTTCCAAAGCCTGCAATGGACCATATATG	1449
Db	373	GGACTGGGAAGAAGGCGAGTCAAGTTTAAACCAAGTCTTTGAAACCTCAANTATAA	432	Qy	1453	CCTACATGAACAAATTAATCTCAATTTCTAACTTTGTCAAAAGCGAGTTCGGACTCTGATG	1512
Qy	436	ATGAGTATGCCGATGCCAGCTACACAACTGTGTGAAGAAATGCGTCAAGAACAGCCCC	495	Db	1450	CCTACATGAACAAATTAATCTCAATTTCTCAGAGTGTGAGTATCGAGTTGGACTTGGCTGG	1509
Db	433	ATGAATTAATCTGATGCCACCTACACAACTAGTGGAAAGAAATGCGTGAAGGACTGCTC	492	Qy	1513	AAATATACATGGAGCTCTCAAAGAAATGCTAGATGCTGATTTGCTTTAAGACCTTACCAA	1572
Qy	496	TCACAGAGAAAGTTGGTAGAGGAG---ATCTCTCTCACCGAGCCAGCCACAAA	552	Db	1510	AAATATACATGGAGCTCTCAAAGAAATCCTAGATGAGTCCAACTTGTCTGAGAACTCCCGA	1569
Db	493	TCACAGAGAAACATTTGACAGAGAGAAAGAAATTTCCAGAGGTGGAAGCCAGCTCTCAGA	552	Qy	1573	CTACGGTCAGATTAGCCCTCGCCATTGATGTCAACTTTCAGCATCATCAGCAAGTCGACT	1632
Qy	553	CTGCAAGCCACCGGCTGTACACAGTAAAGAAAGCGATGATAAGCCCAACAGAACATT	612	Db	1570	CAGCAATGAGTTGTCTATTTGCCCTTGCATTAACCTTCTGATCATCGACAGTTGGAT	1629
Db	553	CTGCAATGTCTCAAAATATATACCAAAACAGAGACAAATCCAAGCTAAAGACACC	612	Qy	1633	TGTTCAAGGGTTGTGATACACAGATGATTTATGACATGTTGCTTAAGATTTGAAATCCGTTTC	1692
Qy	613	ACTACAGGCTTTGTGGTTTCAAGTCAAAAAGATGCTTTTAAACAGATCTTTAAAGCGAA	672	Db	1630	TATTCAGGGCTGTGACACACAGATGATTTATGACCTGCTGAAGTTGAAATCCACTA	1689
Db	613	AAGACA---CGTTTCTTTCAAACCCAGAGAGTCCCAAGTAAAGAGACACCTACGAAGA	669	Qy	1693	TCTATTTGCTGGTGACTTTGTCTGCAAAAGGGAGAAATTTGGCAAGAAATGTATATCA	1752
Qy	673	TTAAACTTCCAAACAGACATAGATTTCATACAGATCGACTCTATCTCTCTGTGGCTTTGC	732	Db	1690	TTATTTACTCTGGTACTTTGTCTGCAAAAGGGAGAAATTTGGAAGAAATGTACATCA	1749
Db	670	TGATCTTTCCAGAGACATAGACTCTTACAGATCGGGTCTATCTCTTGTGGCTCTGCTC	729	Qy	1753	TCAAGCATGGAGAGTCCAAAGTTCTTTGGAGGCCCTGATGTTACTAAAGTTCTGGTTACTC	1812
Qy	733	TTGTCACTTCTTGCCTTAACCTGGAACCTGCTGGTTTATACCACTGCGCTCGTCTTCCAT	792	Db	1750	TCAAAACAGGAGAGTCCCAAGTCTTTGGAGGCCCTGATGGTCTCAAGTTCTTGGTTACTC	1809
Db	730	TTGTCACTTCTTGCCTTAACCTGGAACCTGTTGGTGTCTACCAAGTCCGCTCGTCTTCCAT	789	Qy	1813	TGAAGCTGGGTGCTGGTTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTC	1872
Qy	793	ATCAAAACGAGACAAATACACTACTGCTGCTTATTCGGACATCATATGATATCATCT	852	Db	1810	TGAAGCTGGGTGCTGGTTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAATCGCC	1869
Db	790	GCCAAACACCCAGATAACAGAACTACTGGATTTATCTGACATCGTATGTGATCATCT	849	Qy	1873	GAACTGCCAATGTGGTGGCCACCGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCC	1932
Qy	853	ACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGGAGACATAA	912	Db	1870	GGACAGCTGATGTTGTGGCCCAAGATTTGGCAATCTTTTAACTCTGACAAAAGACTC	1929
Db	850	ACCTTTGATATATCTATTGATCCAGCCAGACTCCAAATTTGTAAGAGGAGGAGAAATTA	909	Qy	1933	TCCAAGAAATTTCTGTGCTATTCGAACTTTTAAAGCTCTCTCATGAAGAAAGCCAAA	1989
Qy	913	TAGTGGATTCMAATGAGCTAAGGAAACACTACAGGACTTCTCAAAATTTTCAAGTTGGATG	972	Db	1933	TGCTTTTAAAGCAGAGGCTTAAGACCGCAGAGCAACCCCTCCCAAGAAAGATCTTGGCC	2052
Db	910	TTGTAGATTCMAATGAGCTAAGGAAACACTACCGAGTTCTTCAAAAGTTTTCGATGGATG	969	Qy	1990	TTCTTTTAAAGCAGAGGAGGAAAGACCACTTCAGGCAATCTCCCTCAAGACACGAGCCTGCT	2049
Qy	973	TGCGATCAATAATACCAATTTGATATTTGCTACCTCTTCTTTGGGTTTAAATCCCAATGTTA	1032	Db	2053	TGCTCTTCCACCGGAAAGAGAGACACCCCAAACTGTTTAAAACTCTCTCTAGGAGGACAG	2112
Db	970	TGGCATCTCTACTGCCATTGGAAGTTCTCTACATCTCTTTGGAGTTTAAATCCCATATTC	1029	Qy	2050	TTCTTTTCCCAACCAAAAGAGAGACACCCGGAATGCTTAAAGTCTCTCTAGGAAACACAG	2109
Qy	1033	GAGCAATAGAGTGTAAAGTACACTCTCAATTTTGAATTTTAAATCATCACTAGAGCTA	1092	Db	2113	GAAAACAGAGTCTTGAAGACTACTCAATTTGAGCGGAGACAGCAGCTCAGAGAAAG	2172

Qy	679	TTCCAAACAGATAGATTTCATACACAGATCGACTTATCTCTGTGGCTCTTCGTTGTCA	738
Db	1988	TTCCCAGAGCAATTGACCCGCTCACCAACTGATGTATGTCTTATGCTCTTCTCGTGG	2047
Qy	739	CTCTGCGCTATAACTGAACTGCTGTTTATACCACTCGCCCTCGCTCCGCCATATCAAA	798
Db	2048	TGATGGCGCTGGAAATTGGAACTGTTGGCTGAATTCCGTGCGCTGGCGCTCCCTACGAGA	2107
Qy	799	CCGAGAGAACATACACTACTCGCTTATTCGGGACATCATATGTGATATCAATCTACCTTT	858
Db	2108	CCCGGACAACTCCACCACTGGCTGTGATGATTACCTATGCGACCTCATCTACTCTCC	2167
Qy	859	ATGATATGCTATTATTCAGCCAGACTCCAGTTTGTAAAGAGAGAGAGACATTAATAGTGG	918
Db	2168	TGGACATCACCGTGTTCACAGACCGCTGCAGTTTGTTCAGAGCGGGGACATCATTACGG	2227
Qy	919	ATTCAAATGAGCTAAGGAAACACTACAGGACTTCTCAAAAATTTCAGTTGGATGTGCGAT	978
Db	2228	ACAAAAGGACATGCGAAATAACTACTCTGAAGTCTCGCCGCTTCAAGATGGACCTGCTCA	2287
Qy	979	CAATAATACCATTTGATATTTGCTACTCTCTTTCTTTGGGTTTATCCAAATGTTTAGAGCAA	1038
Db	2288	GCCTCCCTGCCCTTGGATTTTCTCTATTGTAAAGTCGGTGTGAACCCCTCTCCGCGCTGC	2347
Qy	1039	ATAGGATGTTTAAAGTACACTTCATTTTTCGAAATTAATCATCACTAGAGTCTATAATGG	1098
Db	2348	CCGCTGTTTAAAGTACATGGCCTTCTTCGAGTTTACAGCGCCTGGAAATCCATCTCTCA	2407
Qy	1099	ACAAAGCATATATCTACAGAGTTATTTCGAACAACATGGATACTTGTCTGTTTATTTCGTGACA	1158
Db	2408	GCAAAGCTACGTGTACAGGGTCACTACGAGACCCACAGCCTACTCTCTACAGCGCTGCATT	2467
Qy	1159	TTAATGCCCTGTGTTTATTACTTGGGCTTCAAACTATGAAGAAATGGGCACACTACTAGATGGG	1218
Db	2468	TGAATTCCTGTCTTTATTACTGGGCATCGGCCTATCAGGGCCTCGGCTCCACTCACTGGG	2527
Qy	1219	TGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTATTATTTGGGCAGTTTCGAACTTTAA	1278
Db	2528	TTTACGATGGCTGGGAAACAGTTATATTCGCTGTACTACTTTGCTGTGAAGACCCCTCA	2587
Qy	1279	TTACCATTTGGTGGCTTCCAGAACCAAACTTTATTGTAAATGTTTTTCAACTCTTGA	1338
Db	2588	TCACATCGGGGGGCTGCCTGACCCCAAGACACTTTGTGAAATTTGCTTTCAGCTGCTGA	2647
Qy	1339	ATTTTTTTCTGAGATTTTTTGTGTCTCCAGTTTAAATTTGTTTCAGATGAGAGATGTGATG	1398
Db	2648	ATTATTTACGGGGCTCTTTGCTTTCTCTGTGATGATCGGACAGATGAGAGATGTGGTAG	2707
Qy	1399	GAGCAGCTACAGCCAATCAGAACTACTTCTCGCGCCTGCATGATGACACCATTCGCTTACA	1458
Db	2708	GGGCGGCAACCGCGGAGCAGACCTTACTACCGCAGCTCATGGACAGCACCGTGAAGTACA	2767
Qy	1459	TGAACAATTTACTCCATTCCTTAACTTGTGAAAAGCGAGTTTCGGACTTGGTATGAATATA	1518
Db	2768	TGAATTTCTACAAGATCCCAAGTCGCTGAGAACCCGCTCAAGACCTGGTACGAGTACA	2827
Qy	1519	CATGGGACTCTCAAGAATATGCTAGATGCTGATTTGCTTTAAGACCCCTACCAACTACGG	1578
Db	2828	CCTGGCACTCGCAAGGATGCTGTGATGAGTTCAGAGCTGATGGTTCAGCTTCCAGACAAGA	2887
Qy	1579	TCCAGTTAGCCCTCGCCATTGATGTGAATTCACGATCATCAGCAAAAGTCGACTTGTTC	1638
Db	2888	TGCGGCTGGACCTCGCCATCGAGTGAATCAACATCTGTTAGCAAAAGTCGCACTCTTTC	2947
Qy	1639	AGGGTGTGTATPACACAGATGATTTATGACATGTTTGTCTAAGATTTGAAATTCGGTTCCTATT	1698
Db	2948	AGGGCTGTGACCGGACAGATGATCTTTGACATGCTGAAGAGGCTTCGGCTGTCTGTCTTACC	3007
Qy	1699	TGCGCTGGTACTTTGCTCGCAAAAGGAGAAATTCGCAAGAAATGTATATCATCAAGC	1758
Db	3008	TGCCCAACGACTATGTGTGCAAGAAAGGGGAGATCGGCCGTGAGATGTATCATCATCAGG	3067
Qy	1759	ATGAGAGAAGTCCAAAGTTCTTTGGAGGCCCTGTATGTTACTATAAGTTCTCGTTACTCGAAG	1818

[illegible]

LNYFTGVFAFSWICQMDVUGAATAGATYVRSCHDSTVKYMFYKPKSVQNRVKTW
 XYITHSOMLDESELMVOLDPKMLDIAIDVNNINIVKVALFOGCDROMIFDMLKEL
 RSVYLPNDYVCKGEIEMRYIIOAGQVVLGPDGKSVLITLKAGSVFGBISLLAV
 GGNRRTANVAHGFTNLFILDKKDLNEILVHPESQKLRLKARRMLRSNNPKKEEK
 SVLILPPRAGTFFKLPFNAALMTGKMGKGKAGKLAHLARLKLALALEAAKQOELV
 EOAKSSQDVKEEGSAAPODHTHPKEAATDPAPRTPEPPGSPSPSPASLGRPEG
 BEEGPAEPBEHSVRICMSGPEPGEQILSVKMPERBEKAE"

ORIGIN

Query Match 21.4%; Score 577.4; DB 9; Length 4382;

Best Local Similarity 64.3%; Pred. No. 8.4e-101;

Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

QY	679	TTCCAAACAGCATAGATTCATACACAGATCGACTCTATCTCTGTGGCTCTGTCTGCA 738
DB	1983	TTCCCCAGAGCATTCACCGCTGACCAACCTGATGATGCTCTATGGCTGTCTTCGTGG 2042
QY	739	CTCTTGCCCTATAACTGGAACTGCTGGTTTATACCACATCGCGCTGCTCTTCCCATATCAAA 798
DB	2043	TGATGGCTTGAATTTGGAACCTGTTGCTGATTCCTCGTGGCTTCCCTACCAGA 2102
QY	799	CGCAGACAAATACACTACTGGCTTATGGGACATCATATGATGATATCATCTACCTTT 858
DB	2103	CCCCGGCAACATCCACACATGGCTGCTGATGGATTACCTATGCGACCTCATCTACTTCC 2162
QY	859	ATGATATGCTATTTATCCAGCCCACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGG 918
DB	2163	TGGACATCACCGTGTTCAGACACGCTCGATTTGTTCAGAGGGGGGACATCATTTACGG 2222
QY	919	ATTCAATGAGCTAAGGAAAACACTACAGACTTCTPACAAAATTTCAAGTTGGATTCGCAT 978
DB	2223	ACAAAAGGACATCGGAAATAACTACTCTGAAGTCTCGCGCTTCAAGATGACACCTGCTCA 2282
QY	979	CAATAATACCATTTGCATATTTGCTACCTCTCTTTGGGTTTAAATCAATGTTTAGACAA 1038
DB	2283	GCCTCTCGCTTGGATTTCTTATTTGAAAGTCGGTGTGACCCCTCTCTCGCGCTGC 2342
QY	1039	ATAGATGTTAAAGTACACTTTCAITTTTGAATTTAATCAATCACTAGAGTCTAATATGG 1098
DB	2343	CCCGCTGTTTAAAGTACATGCGCTTCTTCGAGTTTAAACAGCGCTGGAATCCATCTCA 2402
QY	1099	ACNAGCATATATCATACAGACTTATCGAACAATCGATCTCTGTTTATTTCTGCACA 1158
DB	2403	GCAAGCCTACGTGACAGGCTCATCAGGACACAGCTACCTCTCTACAGCCTGCTATT 2462
QY	1159	TTAATGCTGCTGTTTATTTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGG 1218
DB	2463	TGAATCTGCTTTTATTTACTGGCATCGGCTATCAGGCGCTCGCTCCACTCACTGGG 2522
QY	1219	TGATATGATGGGAGGAAACAGATATCTGAGATGTTTATTTGGGAGTTCGAACTTTAA 1278
DB	2523	TTTACGATGGGCTGGGAAACAGTATATATTCGCTGTTACTTCTGCTGTGAAGACCTCA 2582
QY	1279	TTACCATTTGGTGGCTTCCAGAACACAACTTTATTTGAAATTTGTTTCAACTCTTGA 1338
DB	2583	TCACCATCGGGGGCTGCTGACCCCAAGACACTTTTGAATTTGTTTCCAGTCTGTA 2642
QY	1339	ATTTTCTGAGTGGATTTTGTGTTTCTCCAGTTTAAATTTGTCAGATGAGAGATGTGATG 1398
DB	2643	ATTATTTTCAAGGCTGCTTCTGCTGATCGGACAGATGAGAGATGTGATG 2702
QY	1399	GAGCAGCTACAGCAATTCAGAACTACTTCCGCGCTCATGGATGACACCATTCCTTACA 1458
DB	2703	GGGCGCCACCGGGACAGACTTACTACCCAGCTGATGGACAGCAGCGTGAAGTACA 2762
QY	1459	TGAACAATTTACTCCATTTCTTAACTTTGTGAAAACGAGTTCGAGCTTGTATCAATATA 1518
DB	2763	TGAATTTTCAAGATCCCAAGTCCGTCGACAGACCGCTCAAGACCTGTCAGAGTACA 2822
QY	1519	CATGGACTCTCAAGATGCTAGATGCTGATTTGCTTAAAGCCTTACCACTACGAG 1578
DB	2823	CCTGGCACTCGCAAGGATGCTGGATGAGTGAAGCTGATGGTGCAGCTTTCACAGACA 2882

QY	1579	TCAGTTAGCCCTCGCCATTGATGTAAGTCTCAGCATCATCAGCAAAAGTCGACTTGTTC 1638
DB	2883	TGGCGTGGACCTCGCCATCGACGTAACATACAAATCGTTAGCAAGTTCGACTCTTTC 2942
QY	1639	AGGTTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTCTATT 1698
DB	2943	AGGCTGTGACCGGAGATGATCTTTGACATGCTGAAGAGGCTTCGCTCTGTTGCTTACC 3002
QY	1699	TGCTCTGCTACTTGTCTCAAAAAAGGAGAAATTTGGCAAGGAAATGTATATCATCAAGC 1758
DB	3003	TGCCCAACCACTATGTGTGCAAGAGAGGGGAGATCGGCGTGAGATGTACATCATCCAGG 3062
QY	1759	ATGGAAGTCCAAAGTCTTCTGGAGCCCTGATGCTACTTAAAGTCTTGTGTTACTCTGAAAG 1818
DB	3063	CAGGCAAGTGCAGGCTTCTGGGCGGCTGATGGGAAATCTCTGCTGTTGAGCGCTGAAAG 3122
QY	1819	CTGGTCTGCTGTTTGGAGAAATCAGCTTCTAGCAGAGGAGGAGGAAACCGTTCGAACTG 1878
DB	3123	CTGATCTGTTTGGAGAAATAAGCTTCTGCTGCTTGTGGGGCGGGAACCGGCGCACGG 3182
QY	1879	CCAAATGCTGGCCACGCGTTTGGCAATCTTTTAACTCTAGACAAAAGACCTTCCAG 1938
DB	3183	CCAACTGCTGGCGCACGCGTTTACCACTCTTCTATCTGATTAAGAGGACCTGAAATG 3242
QY	1939	AAATCTAGTGCATTCAGATCTGAAAGGATCTCTAAGAGGATCTCATGAAGAAAGCCAGAGTCTTT 1998
DB	3243	AGATTTTGTGCTATCTCTGATCTCAGAGTACTTCGGAAGAAAGCCAGGCGCATGC 3302
QY	1999	TAAAGCAGAGGCTTAAGCCGCGAGAG 2025
DB	3303	TGAGAGCAACAATAAGCCCAAGGAGG 3329

BC045114 4763 bp mRNA linear ROD 16-SEP-2003
 Mus musculus cyclic nucleotide-gated channel beta subunit 1, mRNA
 (CDNA clone IMAGE:4504353), partial cds.

BC045114.1	GI:28175674
Mus musculus (house mouse)	
Mus musculus	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
1 (bases 1 to 4763)	
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Shat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Shieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mialahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, Y., S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.	
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
22388257	
PUBMED	
12477932	
2 (bases 1 to 4763)	
Strausberg, R.	
Direct Submission	
Submitted (27-JAN-2003) National Institutes of Health, Mammalian	

Gene Collection (WGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mc@nih.gov

Contract: nisc.mc@nih.gov

Akhter,N., Aygle,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsungson,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://images.llnl.gov>
Series: IRAC Plate: 85 Row: 1 Column: 9.

FEATURES
SOURCE

```

/organism="Mus musculus"
/mol_type="mRNA"
db_xref="taxon:10090"
clone="INAGB:450433"
tissue_type="Eye, retina,
clone_lib="NH MGC_94"
lab_host="DH10B"
note="vector: pCMV-SPORT6"

```

gene

```
<1. .4763
/gene="Cngb1"
/db_xref="LocusID:333329"
<1. .2602
```

CDS

```

/ gene= "Cngb1"
/ codon_start=2
/ product= "Cngb1 protein"
/ protein_id="AAH5114.1"
/ ab_xref="GI_28175675"
/ db_xref="LocusID:333329"
/ translations="ESEPILVLDSCLVQADVDECOLERTSELASIQELPEKKEKE
EKEKEPEEEEEKEEVESEKKEGKATNSVPAKHEFLPVELVDIADSGDGLPEBTL
PPPEPPPEEEDTETVPGAAAGHKKLQVQDKEBELKALSPASPVVMSDDPTI
PQAKGQDGAASATQNSAI INDRLEQILVFMKERTKVKKFLDPQSDIDSESPKPS
PQAKGQDPAQAKAEVAAEEVEEEDCDMLCKPQKFLDPQSDIDTINVLILW
FFVLVIAAGNCWLIIPVNAFPYQADNIHFWLLMDYLCDIFILDTYFQMLAQVF
LGDIFIDTKMBRNLLKRRKFWMLCILPDLFLYKLGINFLPRLCPRLKVMAPFEF
NRSLEALISKAVYVIRITAYLLYSGLNSCLYVWASAFQISGTSHVDVGVNSYI
RCYVWAKTILITGLPDLTFLVQLNLYFTQVAFQSVIMIGMDVWVGAATAGT
YVYRSCMDSTVKYNVFKYIPRSQNVKQKTYETHSQCMLEDSGLMQLPDKMLDLA
IDNVYSIKVAVLPQCDKQGVFEI SALLVGGNGKRTINVAHGTNFI LDKDNLNEI
QVLGPPGKAVI VTLKAGSFGFII SALLVGGNGKRTINVAHGTNFI LDKDNLNEI
LVHPYSPGKILKKRKAALNRNNKPKKESVLILPPRAGTFLPKAALAAAGAGNGP
AKGKGLAHLRLKILAEALAAQQOOLLEQAKSGAGGEGSGATQDPAQPEPPE
DKPPKPPPEPSPAQSPPPAKPEESTGEAAGPPPSVIRVIRVSPGDPQGTLSVVE
VLEPKKKGAG"

```

misc feature

/gene="Cngb1"
/note="ion trans; Region: Ion transport protein. This family contains Sodium, Potassium, Calcium ion channels. This family is 6 transmembrane helices in which the last two helices flank a loop which determines ion selectivity. In some sub-families (e.g. Na channels) the domain is repeated four times, whereas in others (e.g. K channels) the protein forms a tetramer in the membrane. A bacterial structure of the protein is known for the last two helices but is not the Pfam family due to it lacking

```

the first four helices"
/db_xref="CDD:pfam00520"
1784..2065
/gene="Cngb1"
/note="cNMP_binding; Region: Cyclic nucleotide-binding
domain"
/db_xref="CDD:pfam00027"

```

ORIGIN

Query Match 21.3%; Score 575.2; DB 10; Length 4763;

[illegible]

1139	TGACATCACCGTGTTCAGATGCGCCTCGAGTTTGT	CGAGCGCGGGACATCAITACGG	1199	
919	ATTCAAAATGAGCTAAGGAACAC	CTACAGGACTTCTACAAAA	TTTTCAAGTTGGATGTCGCAAT	978
1199	ACAAAAGGAGATGCGCAACAA	TTACGTGAATCTCAGCGCTTTAAGATGGACATGCTCT	1258	
979	CAATAATACCAATTTGATA	TTTGCTACTCTTTCTTTGGGTTTAATCCAATGTTTAGAGCAA	1038	
1259	GCCTCTTGCCCTTGGACTTACTCTACTTGAAATTCGGTGTGAATCCCTCTCTCGGCTTGC	1318		
1039	ATAGGATGTTAAAGTACACTTCA	TTTTTTTTTGAATTTAATCATCACCTAGAGTCTATAATGG	1098	
1319	CCGCGCTTTGAAGTATATGGCCCTTCTTTGAGTTTAA	CAACCGCCTTGAATCCATCCTCA	1378	
1099	ACAAAGATATATCTACAGAGTTTATTCGAACACTGGATCTTGCTGT	TTATTCTTGCA	1158	
1379	GCAAAGCTACGTTTACAGGGTTATCAGGACCA	CAGCCTACCTGCTCTCAGGTTTACATC	1438	
1159	TTAATGCTCTGTTTATTACTCGGCTTCMAA	CTATGAAGGAA	TTGGCACTTCTAGATGGG	1218
1439	TGA	ACTATGCTTATCTGGCATCGGCTTATGAGGCTCTCGCTCCACTCACTGGG	1498	
1219	TGTATGATGGGAAGGAAACGAGATCTGAGATGTTTATTTAT	TGGCAGTTTCGAACCTTTAA	1278	
1499	TTTATGATGCGTGGGAAACAGATTACATTCGCTGTTACTACTCGGCTGTGAAGACCTCA	1558		
1279	TTACCATGCTGCGCTTCCAGAACCA	CAAACTTTATTTGAAATTTGTTTTTCAACTCTTGA	1338	
1559	TCACCATCGGCGGCTCCCGACCC	CCAGACGCTCTTTGAAATTTGCTTCCAGGGTCTAA	1618	
1339	ATTTTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTTAAT	TGTCAGATGAGAGATGTGATTG	1398	
1619	ACTATTTACGGGCGTCTT	CGCTTCTCGTGATGATCGGACAGATGAGAGAGTAGTGG	1678	
1399	GAGCAGCTACAGCAATCAGAACTACTTTCGCGCGCTGCATGGATGACACCAITTCGCTACA	1458		
1679	GGGCGCGCACCGCGGACAGACCTTACTACCGACGTCGAT	TTGGACAGCACCGTGAAGTATA	1738	
1459	TGAACAAATTA	CTCCATTCCTTAAACTTGTGCAAAAGCGAGTTCGGACTTGTATGAATATA	1518	
1739	TGA	ACTTCTTACAGATCCCAGGTCCTGTCAGAACCGGTCAGACCTGGTACGAATACA	1798	
1519	CATGGGACTCTCAAAGAATGCTAGATGAGTCTGATTTGCTTTAAGACCGCTACCAACTACGG	1578		
1799	CCTGGCACTCCAAAGGATGCTGGATGAGTCAGAGCTGATGGTGCAGCTTTCCGACACAAGA	1858		
1579	TCCAAGTTAGCCCTCGCATTTGATGTGA	ACTTCAGCATCATCAGCAAAAGTCGACTTGTGTCA	1638	
1859	TGCGGCTGGACCTCGCCATTTGACGTGA	ACTTATCCATCGTCAGCAAAAGTGGCACTCTTCC	1918	
1639	AGGGTGTGTGATACACAGATGATTTATGACATGTTTGTCTAAGATTGAAATCCGTTCTCTATT	1698		
1919	AGGGCTGTGACCGGCAGATGATCTTTGACATGCTGGAAGAGCTCGGCTCTGTAGTCTTACC	1978		
1699	TGCGCTGGTGACTTTGTCTGCAAAAGGGAGNAATTTGCAAGGAATCTATATCATCAAGC	1758		
1979	TGCCCAATGATTA	CGTGTGCAAGAAGGGGAGATAGGCGCGGAATATGATCATCATCAGG	2038	
1759	ATGAGAGAGTCCAAAGTTCTTGAGGCGCCTCGATG	TGTTACTTAAAGTTCTCGTTACTCTGAAAG	1818	
2039	CGGGCAGGTGCAGSTCTTGGTGGCCCGGATGGAAATCCGTCGCTGGTACGCTGAAGG	2098		
1819	CTGGGTCGGTGTGTGGAGAAATACGCTTCTTAGCAGCAGGAGAGGAAACCGTGC	ACTG	1878	
2099	CTGGATCTGTGTTTCGGAGAAATAAGCTTGCTGGCTGTAGGGGGCGGGAACCGGCGCACAG	2158		
1879	CCAAATGTGCTGCGCCACCGGTTTGCCAATCTTTTAACTCTAGACAAAAAGACCTTCCAAG	1938		
2159	CTAACGTTGGTGGCCCATGGGTTTACCACTTCTTCATTTCTGGATAGAGGACCTG	ACTG	2218	
1939	AAATTTCTAGTGCATATCCAGATTTGTAAAGATCCCTCATGAGAAAGCCGAGATGCTTT	1998		
2219	AAATTTCTGGTGCATATCCCGAGTCTCAGAAGTTGCTCCGCAAGAAGGCCAGGCGAATGC	2278		

Qy	1999 TAAAGCAGAAGGCTATAGACCGCAGA	2023
Dd	2279 TGAGAAATCAACAAGCCCAAGGA	2303
RESULT 13		
LOCUS	AF074014	
DEFINITION	Bos taurus cyclic nucleotide-gated channel beta subunit le (CNCBeta) mRNA, complete cds.	
ACCESSION	AF074014	
VERSION	AF074014.1	GI:3309625
KEYWORDS		
SOURCE	Bos taurus (cow)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
REFERENCE	Bovidae; Bovinae; Bos. 1 (bases 1 to 3290) Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and Weinand,I. Cyclic nucleotide-gated channels on the flagellum control Ca ²⁺ entry into sperm J. Cell Biol. 142 (2), 473-484 (1998)	
MEDLINE	98345361	
PUBMED	9879145	
AUTHORS	2 (bases 1 to 3290) Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and weinand,I. Direct Submission Submitted (24-JUN-1998) IBI, FZ-Juelich, Leo-Brandt-Strasse, Juelich, NRW 52425, Germany	
TITLE	Location/Qualifiers 1..3290 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913"	
FEATURES	source 1..3290 /gene="CNCBeta" 200..3058 /gene="CNCBeta" /codon_start=1 /product="cyclic nucleotide-gated channel beta subunit le" /protein_id="AAC26129.1" /db_xref="GI:3309625" translation="MNVIAPLSSCIMASLIAKTARPHNSVLDSYLVPSBEDRSEEE ETDQSVGGQAQDEVGGAQALSEESETQDSVEVGGQAQDEVGGAQAEVGGQAQ EQDVGGQAQDSHQLQEELADSGVPATEEHPPELQVEDADADRPLIAENPSPQS VOLFLPAKSTAVSLAPGSATGLRKRLPSQDDEAELMLSPAAPSYYVAWDPTSPQS TDODRASTFASONSAINDRLOBLVKLFKERTKEVKELIDPDVTSEESPCKPSPAL KAPFAEPVPAEGAVEEHYCEMLCCKFKRRPWKYQFPQSDLPDLNLMYLWLF VTLAWNWCWLIPVRAPFYPTDPNIHLWLLMDYLCDLIYLLDITVFOMLQFVRGG IIITDKERNRNYSQRPKMLCLLDLLLYLKFGPNLLRLKCLMKAMAFFENNRI LESLIKAYVYRVIRTTAYLLSHLSNCLYXWASVEGLSTHWVGVGNRSIRCI YWAKTLITIIGLDPDRTLFIIVFQGLNYFTGFVAFYSIMQMRDVDGAATAGTYIY SCMDTSVMNMFWYKI PRSQNRVKTWEYTWHSQCMLDES ELMTQLPKMRILDLAI NYSLVKVALPQGCDROMI PMLKLRSVVYLPNDYVCCKGEIGREMYII OAGQVYI GGPGKSVLITLKGSPGETSILLAVGGNERRTANVAHGFTNLFILCKKOLNEILV YPESOKLURKKAERLRNNRPKESVLLIPPRAGTPKLFNAALAAGMGAKGGRG RLALLRLKELALEAROQQLEQLAESSEDAAVGEESGASPQP RPPEPPAPEAE APEPTAPEPLAAPAPAPSPPPPASPQRPPEGCDKDAARPEHPRIHVLTGDPDF FOILLVEYPKEOEKKEEKETEKEEARKKEEF"	

ORIGIN			
Query Match	21.2%;	Score 572.2;	DB 4; Length 3290;
Best Local Similarity	64.11%;	Fold No. 8.6e-100;	
Matches 862;	Conservative	0; Mismatches 483;	Indels 0; Gaps 0
QY	679	TTCCAAACAGGCATAGATTATACACAGATCGACTCTATCTCTGTGGGCTTGGCTTGCA	738
Db	1146	TTCCCGAGAGATCGACCGGTGACCAACTGATGATACATCTGTGGGTGTCTTCGTGG	120


```
QY 739 CTCTTGGCTTAATGGAAGTCTGTTTATACCACTGCGCTCTCTCCCATATCAAA 798
Db 1206 TGTGCGCTTGAAGTCTGGAAGTCTGTTTATACCACTGCGCTCTCTCCCATATCA 1265
QY 799 CCGCAGACATACATACCTACTGCTTATTCGGGACATCATATGTGATATCATCTACCTTT 858
Db 1266 CGCCAGACATACATACCTACTGCTTATTCGGGACATCATATGTGATATCATCTACCTCC 1325
QY 859 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGAGACATAATAGTGG 918
Db 1326 TGGACATACCTGTTTCCAGATCGCGCTCGAGTTTGTTCAGAGCGGGGACATCATACGG 1385
QY 919 ATTCAATGAGCTTAAGGAACACTCAGGACTTCTACAAATTTTCAGTTGGATGTCGAT 978
Db 1386 ACAAAGAGATGCGCAATATGCTGAATCTCAGCGCTTTAAGATGGACATGCTCT 1445
QY 979 CAATAATACATTTGATATTTGCTACTCTCTCTTGGGTTAATCCAAATGTTTGAAGCAA 1038
Db 1446 GCTCTTGGCTTGGACTTACTTCTACTTGAATTCGGTGTGAATCCCTCTGCGCTTGC 1505
QY 1039 ATAGGATGTTAAGTACACTTCTATTTTGAATTTTAAATCATCACCTAGACTTAAATGG 1098
Db 1506 CCGCTGTTTGAAGTATATGGCTCTCTTGAATTTTAAACACCGCTGGAATCCATCTCA 1565
QY 1099 ACAAGCATATATATACAGAGTTATTCGAACACTTGGATCTGCTGTTTATCTGCACA 1158
Db 1566 GCAAGGCTTACGTTTACAGGGTATCAGGACACAGCTTCTCTACAGCTTACATC 1625
QY 1159 TTAATGCTGTTTATTTACTGGCTTCAACTATGAAGGAATTTGGCACTACTAGATGGG 1218
Db 1626 TGAACATGCTCTTATTTACTGGGATCGGCTATGAGGCGCTCGGCTCCACTCACTGGG 1685
QY 1219 TGTATGATGGGGAAGGAACGAGTATCTGAGATGTTATTTATGGGAGTTCGAACTTTAA 1278
Db 1686 TTATGATGGCTGGGAACAGTTACTGCTGTTTACTTGGGCTGTGAAGACCTCA 1745
QY 1279 TTACATTTGGCTTCCAGAACACAACTTTTATTTGAATTTTTCAACTTTTGA 1338
Db 1746 TCACCATCGCGGCTTCCGAGCCAGAGCTCTTTGAAATTTCTTCCAGGCTCAA 1805
QY 1339 ATTTTCTTGGAGTTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1398
Db 1806 ACTATTTACGGGCTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1865
QY 1399 GAGCAGCTACAGCAATCAGAACTACTTCCGCGCTGATGATGATGACACCACTTCCCTACA 1458
Db 1866 GGGCGCCACCGCGGACAGACCTACTACCGCAGCTGATGATGATGATGATGATGATGAT 1925
QY 1459 TGAACAATTTACTTCTTAACTTTGTGAAAGAGGAGTTCGAGCTTGGTATGATGATGAT 1518
Db 1926 TGAACCTTCTACAGATCCCGAGTCCGTCGAGAACCGGGTCAAGACCTGATGATGATGAT 1985
QY 1519 CATGGGACTCTCAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATGATGAT 1578
Db 1986 CTTGCACTTCCAGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2045
QY 1579 TCCAGTTAGCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1638
Db 2046 TCGGCTGATCTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2105
QY 1639 AGGTTTGTGATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1698
Db 2106 AGGCTGTGACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2165
QY 1699 TGCCTGTGATTTTGTTCGAAAGGAGAAATTTGCAAGAAATGATATATATCAATCAAGC 1758
Db 2166 TGCCCAATGATTTAGTGTGCAAGAGGAGGAGATAGGCGGGAATGTATCATCTCAGG 2225
QY 1759 ATGAGAGAGTCCAAGTTCTTGGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 1818
Db 2226 CGGGCAGGTCAGGTTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGGTTGGG 2285
QY 1819 CTGGGTCGGTTTGGGAAATCAGCTTCTTAGCAGGAGGAGGAGGAAACCGTCGAATG 1878
```

```
Db 2286 CTGATCTGTGTTCCGAGAAATAAGCTTGTGCTGTAGGGCGGGAACCGCGCACAG 2345
QY 1879 CCAATGTGGTGGCCCGGCTTTGCCAATCTTTAACTCTAGACAAAGAGCCTCAAG 1938
Db 2346 CTAAGTGTGGCCCGGCTTTTACCACTCTTCTTCTGATTAAGAGAGCCTGAATG 2405
QY 1939 AAATTTAGTGCATTATCCAGATTTCTGAAGGATCTCATGAAGAGGACAGAGTCTTT 1998
Db 2406 AAATTTAGTGCATTATCCGAGTCTCAGAAGTTGCTCGCAAGAGGCGGCGAATGC 2465
QY 1999 TAAAGCAGAGGCTTAAGCGCAGA 2023
Db 2466 TGAGAAATAACAACAGCCCAAGGA 2490

RESULT 14
BTRPCNGCL
LOCUS B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.
DEFINITION B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.
ACCESSION X89626
VERSION X89626.1 GI:1050440
KEYWORDS beta subunit; CNG channel; rod photoreceptor.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactylia; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1
AUTHORS Koerschen,H.G., Illing,M., Seifert,R., Sesti,F., Williams,A.,
Gotzes,S., Colville,C., Muller,F., Dose,A., Godde,M., Molday,L.,
Kaupp,U.B. and Molday,R.S.
A 240 kDa protein represents the complete beta subunit of the
cyclic nucleotide-gated channel from rod photoreceptor
Neuron 15 (3), 627-636 (1995)
96009859
7546742
REFERENCE 2 (bases 1 to 4282)
AUTHORS Kaupp,U.B.
Direct Submission
Submitted (12-JUN-1995) U.B. Kaupp, Forschungszentrum Juelich,
Institut fuer Biologische, Informationsverarbeitung, Postfach 1913,
52425 Juelich, FRG
FEATURES
Location/Qualifiers
1..4282
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
43..4227
/note="beta subunit"
/codon_start=1
/product="240K protein of rod photoreceptor cng-channel"
/protein_id="CAA61769.1"
/db_xref="GI:1050441"
/db_xref="GOA:Q28181"
/db_xref="SWISS-PROT:Q28181"
/translation="MLGVQVLPQPCTPQTKOEBEGTEPELEPKPAPETE
LEEVLPPEPCVCGKEVAATLPGQGTETALTPTLSQAVSVAPSAHSPRGVLT
WURKGVKVPQVAPSHSRPPIAAGLESPPQQAQILGCGTGGSDGSEPRGAE
PPGFWLLWFEONLEKMLPPPKISEGRDEPTDAALGPPPGPALIKMLQAOES
PSLAPGPPEEPPIPEPTQASLLPPQDSARULMATHLEMLPQVIRGK
GQESDAPVTCVQTSILPQGESHLILEVDPHWEEDHQGSTSTSPRTSEAP
ADEEGKVVQTPRELPRIOKEDEEBEKEDEEBEKEDEEBEKEDEEBEKEE
KEEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKE
VEGREDEEBEKEDEEBEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKE
LSEESVQDQSEVGQAQSEVGQAQSEVGQAQSEVGQAQSEVGQAQSEVGQAQ
ADSSQVATEHEPQVEDADSRPLIAENPPSPVQLPLSPAKSDTLAVPGSATG
LRLKPSODDSEAEELKMLSPAASPVVWSDTSPQGTDDQDRASTASQSAIINDL
CELVLKFERTEKYKEKILIDPVTDSDESPKPAKPAPEPAKPAKPAKPAK
CEMLCKFRPWRPKIQFPIDPLTNLMYILMLFFVVLAWNWCWLPVWPAEYQY
PNIHLMLMDYLCDLIYLLDITVQMLQFVRGDIITDKERNRYVKSQPMQD
LCLELDLILYKFGVNPILRLPRCLMAFEFNRLLESILSKAYVYVIRITLYLY
SLHNSCLYYWASVEGLGTHWVYDGVGNSYIRCYWAVKTLITIGLDPDPTLFEI
```

VFOGLAVFTCVAFSPVMI COMEDRVGAATAGTQTVYBSOMDSTYKMYNFKJ PRSVQNO
 VKYVYVTHSOSGVMICEDRVGKPKWRLDADLVNYSVSKVAFQCGDGRMD FDM
 LKLVRSVYLPNDVPGCKEIGREMYIQAQGVOLKQVSGKLVLTAKGSVFGNIS
 LLVAGSNGRTANVAGHTNPIFLDKLQNEILVHPYESOKILRKWARMLENNKPS
 KESVLIPLPRACTKJFNVALAAAGKMGKAGRGCRILLARLKLALAEAAQAOQ
 QLEQKASKEEDAAVGEESGASPEOPREPPAPAEPAPEPTAPLEPLAEAPAPAP
 SSTSPASORPEDGDKAARPESHVRHVHTVCPDPSQIILVVEVPQEEKEKEEBT
 EEKEEPEARKEEES"

ORIGIN

Query Match	21.2%	Score 572.2;	DB 4;	Length 4282;
Best Local Similarity	64.1%	Pred. No. 8.4e-100;		
Matches 862;	Conservative	0;	Mismatches 483;	Indels 0;
				Gaps 0;

QY	679	TTCCAAACACGATAGATT	CATACACAGATCGACT	CTATCTCCTGTGCTCTTGCTTGCTCA	738
DB	2315	TTCCCCAGAGCATCGA	CCCGCTGACCAACTGAT	GTACATCTTGCTGCTGTTCTTCTGTGG	2374
QY	739	CTCTTGCTCTATAACT	GTGAATCTGCTGTTTAT	TACCACTCGCGCTCGTCTTCCCATATCAAA	798
DB	2375	TGCTGGCTCGGA	ACTGTGCTGGCTGAT	TCCCGTGGCTGGCGCTTCCCTCATCAGA	2434
QY	799	CCGAGACACATACACT	ACTTGGCTTATTCGGGACATCATAT	GTGATATCATCTACCTCTT	858
DB	2435	CGCCAGACACATCCAC	CTCTGGCTGCTGATGGA	TACCTGTGTGACCTCATCTACCTCC	2494
QY	859	ATGATATGCTATTAT	TATCCAGCCACAGCT	CCAGTTTGTAAAGGAGGAGACATATAGTGG	918
DB	2495	TGGACATACCGTGT	TCAGATGCGCTCGATTTGT	TCAGAGCGGGGACATCATTAACG	2554
QY	919	ATTCAAATAGCTAAG	GAACACCTACAGGACTTCT	CACAAATTTTCAGTTGGATGTCCGAT	978
DB	2555	ACAAAAGGAGATGCG	CAACAATACGTGAAAT	CTCAGCGCTTTAAGATGACATGTCT	2614
QY	979	CAATAATACCAATTT	GATATTGCTACCTCTT	CTTTGGTTTAAATCCCAATGTTTAGAGCAA	1038
DB	2615	GCCTCTTGCCTTGG	ACTTACTCTTGAAATTCGG	TGTGAAATCCCTCTCTCGCTTGC	2674
QY	1039	ATAGAGTTTAAAGT	ACACTTTCATTTTGAATTTAAT	CATCACTAGAGTCTATAATGG	1098
DB	2675	CCCGCTGTTGAAG	TATATGSCCTCTTTGAGTTT	TAAACCGCTGGAATCCATCTCA	2734
QY	1099	ACAAAGCANATATCT	CACAGATTATCGAA	CAACTGGATCTTCTGTGTTATCTGCACA	1158
DB	2735	GCAAAGCCTACGTTT	TACAGGGTTATCAGGA	CCACAGCCTACTGCTCTACAGCTTACATC	2794
QY	1159	TTAATGCTGTGTTTAT	TACTGGGCTTCAAACTATGA	AGGAATTTGGCACTACTAGATGGG	1218
DB	2795	TGAATCATGTCTCTAT	CTTACTTGGGCATCGGC	TATGAGGGCTCGCTCCACTCACTGGG	2855
QY	1219	TGTATGATGGGAAG	GAAGATCTGAGATGTTAT	TATTTGGGCAGTTTCGAATTTAA	1278
DB	2855	TTTATGATGGCGTGG	AAACAGTTACATTCGCTGTTACT	CTGGGCTGTGGAAGACCTCA	2914
QY	1279	TTACATTTGGTGGCT	CTCCAGAACACAAATTTTAT	TTTGAATTTTCTTCAACTCTTGA	1338
DB	2915	TCACCATCGGGCGCT	CGCCGACCCAGGACGCTCT	TTTGAATTTCTTCAGGGTCTAA	2974
QY	1339	ATTTTCTTGAGT	TTTTTGTGTTCTCCAGTTTAA	TTTGGTCAGATGAGAGATGATG	1398
DB	2975	ACTATTTCA	CGGCGCTCTTCGCTTCTCCG	TATGATCGGACAGATGAGACGCTAGTGG	3033
QY	1399	GAGCAGCTACAGC	CAATCAGAACTACTTTCGGCGCTGCAT	CGATGACACCAATTCGCTACA	1455
DB	3035	GGGGCCGACCCGCG	GAAGACCTTACTACCGCAGCTGCAT	GTGACAGACCGCTGGAAGTATA	3095
QY	1459	TGAACAATTTACTCC	ATTCTCTAAATTTGTGCAAAAGCAG	TTCCGGACTTGGTATGAATATA	1515
DB	3095	TGAATTTCTAC	AGATCCCAGGTCGTCGAAACCG	GTCAAGACCTGGTACGAATACA	3155
QY	1519	CATGGGACTCTCAA	AGATGCTAGATGTGATTTGCTT	TAAGACCTTACCACTACGG	1575
DB	3155	CTGTGCATCTCCAA	GGCATGCTGGATGATGTAGAGTCA	GAGCTGATGTGCGGACAGA	3215

1579	TCGAGTTAGCCCTCGCCATTGATGTGAACCTTCAGCATCATCAGCAAGTCGACTTCTTCA	1633
3215	TGGCGTGCACCTCGCCATTGACGTGAACATTCCCATCGTCAGCAAGTGGCACTCTTCC	3274
1639	AGGGTTGTGATACACAGATGATTTATGACATGTTGTAAAGATTGAAATCCGTTCTCTATT	1698
3275	AGGCTGTGACCGGCAGATGATCTTTGACATGCTGAAGAGCTCGCTCTGTAGTCTACC	3334
1699	TGCCTCGTGACTTTGTCTGCAAAAGCGGAGAAATTTGGCAAGGAAATGTATATCATCAAGC	1758
3335	TGCCCAATGATTACGTTGTGCAAGAGGGGAGATAGGCGGGAAATGTATCATCATCAGG	3394
1759	ATCGAGAAGTCCAAAGTTCTTGGAGGCCCTCATGCTACTAAAGTTCTGGTTACTCTGAAAG	1818
3395	CGGGCAGGTGCAGTCTTGGTGTGCCGGATGGGAAATCCGTCGTGGTCAGCTGAAG	3454
1819	CTGGTCTGGTGTTTGGAGAAATCAGCCTTCTACAGCAGAGAGAGAAACCGTCGAACCTG	1878
3455	CTGGATCTGTGTTTCGGAGAAATAAGCTTGTGGCTGTAGGGGCGGGAACCGGCGCACAG	3514
1879	CCAAATGTGTGGCCACGGGTTTGGCAATCTTTTAACTCTAGACAAAGAGCCCTCCAAAG	1938
3515	CTAACGTGTGGGCCATGGGTTTACCAACTCTTCATTCTGGATAGAGAGACCTGTAATG	3574
1939	AAATTCTAGTGCAATTATCCAGATTCTGAAAGGATTCCTCATGAAGAAAGCCAGAGTGTCTT	1998
3575	AAATTCTGGTGCAATTATCCGAGTCTCAGAAAGTTGCTCCGCAAGAGCCAGCGGAATGC	3634
1999	TAAAGCAGAAGGCTTAAGACCGCAGA	2023
3635	TGAGAAATAACAAACGACCCCAAGA	3659

RESULT 15

RNCNG41	RNCNG41	4238 bp	linear	ROD 02-MAR-1998
LOCUS	Rattus norvegicus mRNA for cyclic nucleotide-gated cation channel		beta subunit.	
DEFINITION				

AJ000496
 AJ000496.1 GI:2292985
 beta subunit; CNG4.1 gene; cyclic nucleotide-gated cation channel.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE	1	Sautter, A., Biel, M. and Hofmann, F.
AUTHORS		
TITLE		Molecular cloning of cyclic nucleotide-gated cation channel subunits from pineal gland
JOURNAL		Mol. Brain Res. 47, 171-175 (1997)
REFERENCE	2	(bases 1 to 4238)
AUTHORS		Sautter, A.

TITLE
JOURNAL
Direct Submission
Submitted (17-JUL-1997) Sauter A., Institut f. Pharmakologie u.
Toxikologie, Technische Universitaet Muenchen, Biedersteiner Str.
29, D-80802 Muenchen, GERMANY

FEATURES	source	Location/Qualifiers
		1..4238
		/organism="Rattus norvegicus"
		/mol_type="mRNA"
		/strain="Sprague-Dawley"
		/db_xref="taxon:10116"
gene		1..4238
		/gene="CNG4.1"
CDS		59..4078
		/gene="CNG4.1"
		/codon_start=1
		/product="cyclic nucleotide-gated channel beta subunit"
		/protein_id="CAA04133.1"
		/db_xref="GI:2292986"
		/db_xref="GOA:O35788"

— 2 —

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 17:15:00 ; Search time 1007.37 Seconds
(without alignments)
11398.850 Million cell updates/sec

Title: US-09-855-828-2
Perfect score: 2703
Sequence: 1 cattctctacctaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002s.*
7: Geneseq2003as.*
8: Geneseq2003bs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	2757	6	Aad25729 Human cyc
2	654.4	24.2	2516	5	Aas63653 DNA encod
3	577.4	21.4	2607	7	Abz80565 Nucleotid
4	573.6	21.1	3811	5	Aas91658 DNA encod
5	569.6	21.2	4238	9	Adb53355 Primary r
6	518	19.2	2244	5	Aas76156 DNA encod
7	518	19.2	2244	5	Aas76184 DNA encod
8	223	8.3	3275	4	ABL19457 Drosophil
9	176.4	6.5	2500	9	Adg93243 Cyclic nu
10	160.6	5.9	289	5	Aas75291 DNA encod
11	136.2	5.0	2109	4	ABL18085 Drosophil
12	132.8	4.9	3486	9	Aad58492 Human CNG
13	131.6	4.9	1995	7	Aad56241 Rat CNG c
14	131.6	4.9	1995	7	Aad56239 Rat CNG c
15	129	4.8	526	4	Abz61898 Human foe
16	129	4.8	526	4	AAI41823 Probe #10
17	129	4.8	526	4	AAK36108 Human bon
18	129	4.8	526	4	AAK10209 Human bra
19	129	4.8	526	4	ABS35801 Human liv
20	128.4	4.8	1995	7	Aad56242 Rat CNG c
21	128.4	4.8	1995	7	Aad56240 Rat CNG c
22	127	4.7	127	4	ABA74393 Human foe
23	127	4.7	127	4	AAI54858 Probe #23

ALIGNMENTS

RESULT 1
AAD25729
ID Aad25729 standard; DNA; 2757 BP.

AC Aad25729;

DT 26-MAR-2002 (first entry)

XX Human cyclic nucleotide-gated cation channel 3 beta subunit DNA.

XX Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
XX cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
XX male infertility; Genetic defect; reporter-ligand interaction; CNG;
XX viral infection; cancer; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc_feature 1...49

FT /tag= a

FT /note= "These bases are absent in the sequence shown as
SEQ ID NO:2 in Page 64-65 of the specification"

FT CDS 112...2541

FT /tag= b

FT /product= "Human CNG3B protein"

FT /note= "This region is specifically claimed in claim 4 as
SEQ ID NO:4"

FT misc_feature 2753...2757

FT /tag= c

FT /note= "These bases are absent in the sequence shown as
SEQ ID NO:2 in Page 64-65 of the specification"

XX WO200188090-A2.

XX 22-NOV-2001.

XX 15-MAY-2001; 2001WO-US015814.

XX 15-MAY-2000; 2000US-0204445P.

XX 14-MAY-2001; 2001US-00855828.

XX (ICAG-) ICAGEN INC.

XX Creech CD, Jegla TJ;

XX WPI; 2002-089847/12.

24 127 4.7 127 4 AAK49030 Human bon
25 127 4.7 127 4 AAK22857 Human bra
26 127 4.7 127 4 ABS48687 Human liv
27 124.4 4.6 5133 4 ABL14931 Drosophil
28 120.6 4.5 5692 4 ABL19456 Drosophil
29 116.8 4.3 1989 7 ABX94804 Bovine CN
30 115.2 4.3 1989 7 ABX94805 Bovine CN
31 113.6 4.2 1989 7 ABX94806 Bovine CN
32 111.2 4.1 1995 6 ABQ78297 Human tra
33 111.2 4.1 1995 6 ABQ78297 Nucleotid
34 111.2 4.1 1995 6 ABS58301 cDNA enco
35 111.2 4.1 1995 7 ABZ80563 Human NOV
36 111.2 4.1 2111 7 ABX56269 Variant H
37 111.2 4.1 2190 6 ABA00289 Novel hum
38 111.2 4.1 12017 7 ABS58302 Nucleotid
39 109.6 4.1 2186 6 ABA00288 HbMYCNG C
40 109.6 4.1 3080 7 ACC43832 Nucleotid
41 96.4 3.6 2809 4 ABL13353 Drosophil
42 86.8 3.2 1281 4 ABL06311 Drosophil
43 85.6 3.2 2223 2 AAQ29187 cDNA enco
44 85.6 3.2 2223 2 AAQ80908 Plasmodiu
45 83 3.1 372 5 AAS75452 DNA encod

DR P-PSDB; AAE15982.
 XX New polypeptide, useful for screening for modulators of cyclic nucleotide-
 PT -gated ion channels, comprises the isolated cyclic nucleotide-gated
 PT cation channel 3 beta subunit.
 XX Claim 4; Fig 2; 83pp; English.
 XX The invention relates to human cyclic nucleotide-gated cation channel 3
 CC beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
 CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
 CC functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
 CC subunits that are expressed in retina. CNG3B polypeptides are useful for
 CC screening modulators of CNGs which are useful as contraceptives and for
 CC treating various disorders involving cation channels, e.g. vision
 CC disorders and male infertility. Polynucleotides of the invention are
 CC useful for transfection of cells in vitro and in vivo, to correct
 CC acquired and inherited genetic defects, cancer and viral infections.
 CC Sequences of the invention are useful as reporter molecules in assays and
 CC detection systems, to measure changes in cation concentration, membrane
 CC potential, current flow, ion flux, transcription, signal transduction,
 CC reporter-ligand interactions and second messenger concentrations, in
 CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs
 CC in a computer system and for examining expression and regulation of
 CC cation channels. The present sequence is a DNA encoding CNG3B protein
 XX Sequence 2757 BP; 946 A; 571 C; 581 G; 659 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 2703; DB 6; Length 2757;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2703; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATTTCTCTACCTTAAGCCAGCTGATTAATACAGAGGTTTTCAGAACCACTCCAGAGA 60
 DB 50 CATTTCTCTACCTTAAGCCAGCTGATTAATACAGAGGTTTTCAGAACCACTCCAGAGA 109
 QY 61 AGATGTTTAAATCGCTGCAAAAGTCAACAAAGTGAAGCCCTATAGGAGAGAAACAATGAGA 120
 DB 110 AGATGTTTAAATCGCTGCAAAAGTCAACAAAGTGAAGCCCTATAGGAGAGAAACAATGAGA 169
 QY 121 ATGACAAAGTCTCGTGGATGAGAGAGCTCTCACCAGTAATCACTCTCAGCAAA 180
 DB 170 ATGACAAAGTCTCGTGGATGAGAGAGCTCTCACCAGTAATCACTCTCAGCAAA 229
 QY 181 CCACAGCAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAG 240
 DB 230 CCACAGCAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAG 289
 QY 241 TCAGTCTGAAGAGCCACACACACATACAGACAACTCTCAGAGAAATTCCTCTG 300
 DB 290 TCAGTCTGAAGAGCCACACACACATACAGACAACTCTCAGAGAAATTCCTCTG 349
 QY 301 GAGATCTGACCAACAAACCTGACCTCAAAATGAGAGAGAACTGGAACAGTGCAG 360
 DB 350 GAGATCTGACCAACAAACCTGACCTCAAAATGAGAGAGAACTGGAACAGTGCAG 409
 QY 361 AGCAGAGAAATGAGACCCGGGAAAGAGTCCAAACAGCCCAACAAACACCGCTG 420
 DB 410 AGCAGAGAAATGAGACCCGGGAAAGAGTCCAAACAGCCCAACAAACACCGCTG 469
 QY 421 CAGTCTCTGTTTAAATGAGTATGCCGATGCCAGTACCAACTGGTCAAAAGATGC 480
 DB 470 CAGTCTCTGTTTAAATGAGTATGCCGATGCCAGTACCAACTGGTCAAAAGATGC 529
 QY 481 GTCAAGAACAGCCCTCTCAAGAAAGATGTTGGTAGAGGAGATCTCTCTCAACCGAAG 540
 DB 530 GTCAAGAACAGCCCTCTCAAGAAAGATGTTGGTAGAGGAGATCTCTCTCAACCGAAG 589
 QY 541 CCAGCCCAACAACTGCAAGCCACGGCTGTPACCACAGTAAAGAGAGCGATGATAAGC 600
 DB 590 CCAGCCCAACAACTGCAAGCCACGGCTGTPACCACAGTAAAGAGAGCGATGATAAGC 649
 QY 601 CAACAGAACATTTACTACAGGCTGTTGTTGTTTCAAAAGTCAAAAGATGCTTTTAAACAGAGT 660

DB 650 CAACAGAACATTTACTACAGGCTGTTGTTGTTTCAAAAGATGCTTTTAAACAGAGT 709
 QY 661 ACTTAAAGCGAATTTAAACTTTCAAAACAGCATAGATTCATACACAGATCGACTCTATCTCC 720
 DB 710 ACTTAAAGCGAATTTAAACTTTCAAAACAGCATAGATTCATACACAGATCGACTCTATCTCC 769
 QY 721 TGTGGCTCTTGTGTGCTCACTCTTGGCTATAAATGGAACCTGCTGGTTTATACCACTGCGCC 780
 DB 770 TGTGGCTCTTGTGTGCTCACTCTTGGCTATAAATGGAACCTGCTGGTTTATACCACTGCGCC 829
 QY 781 TGTCTCTTCCATATCAAAACCGAGACAACTACTCTGCTTATTCGGGACATCATAT 840
 DB 830 TGTCTCTTCCATATCAAAACCGAGACAACTACTCTGCTTATTCGGGACATCATAT 889
 QY 841 GTGATATCATCTACCTTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAG 900
 DB 890 GTGATATCATCTACCTTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAG 949
 QY 901 GAGGACACATAATGCTGGATTCAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAT 960
 DB 950 GAGGACACATAATGCTGGATTCAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAT 1009
 QY 961 TTCAGTTGGATCTCGCATCAATAATACCAATTTGATATTTGCTTACCTCTCTTTGGGTTTA 1020
 DB 1010 TTCAGTTGGATCTCGCATCAATAATACCAATTTGATATTTGCTTACCTCTCTTTGGGTTTA 1069
 QY 1021 ATCCATGTTTAGACAAATAGATGTTTAAAGTACACTTCTTTTGAATTTATCATC 1080
 DB 1070 ATCCATGTTTAGACAAATAGATGTTTAAAGTACACTTCTTTTGAATTTATCATC 1129
 QY 1081 ACTTAGAGTCTTAATGGAACAAAGCATATATCTACAGAGTTTATTCGAAACAACTGATACT 1140
 DB 1130 ACTTAGAGTCTTAATGGAACAAAGCATATATCTACAGAGTTTATTCGAAACAACTGATACT 1189
 QY 1141 TGTGTTTAAATCTGACATTAATGCTGTTTATTTACTGGGCTTCAAACTATGAAGAA 1200
 DB 1190 TGTGTTTAAATCTGACATTAATGCTGTTTATTTACTGGGCTTCAAACTATGAAGAA 1249
 QY 1201 TTGGCACTACTAGATGGGTGATGATGGGAGGAAACAGATATCTGAGATGTTTATTT 1260
 DB 1250 TTGGCACTACTAGATGGGTGATGATGGGAGGAAACAGATATCTGAGATGTTTATTT 1309
 QY 1261 GGGCAGTTTCAAACTTAAATACCATTTGGTGGCTTCCAGAACCAAACTTTATTTGAAA 1320
 DB 1310 GGGCAGTTTCAAACTTAAATACCATTTGGTGGCTTCCAGAACCAAACTTTATTTGAAA 1369
 QY 1321 TTGTTTTCAACTCTGAAATTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATGGTC 1380
 DB 1370 TTGTTTTCAACTCTGAAATTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATGGTC 1429
 QY 1381 AGATGAGAGATGATGTTGGAGAGCTACAGCAATCAGAACTACTTCCGCGCTGCATGG 1440
 DB 1430 AGATGAGAGATGATGTTGGAGAGCTACAGCAATCAGAACTACTTCCGCGCTGCATGG 1489
 QY 1441 ATGACACCAATTCCTTACATGAAACATTTACTCCATTTCTTAACTTTGTGCAAAAGGGAGTTC 1500
 DB 1490 ATGACACCAATTCCTTACATGAAACATTTACTCCATTTCTTAACTTTGTGCAAAAGGGAGTTC 1549
 QY 1501 GGACTTGGTATGAATATACATGGAAGCTCTCAAGAAATCTAGATGAGTCTGATTTGCTTTA 1560
 DB 1550 GGACTTGGTATGAATATACATGGAAGCTCTCAAGAAATCTAGATGAGTCTGATTTGCTTTA 1609
 QY 1561 AGACCCCTACCAACTACCGTCCAGTTAGCCCTCGCCATTTGATGTAACCTCAGCATCATCA 1620
 DB 1610 AGACCCCTACCAACTACCGTCCAGTTAGCCCTCGCCATTTGATGTAACCTCAGCATCATCA 1669
 QY 1621 GCAAAAGTGCATTTGTTCAAGGGTTCGTATACACAGATGATTTTATGATGTTGCTAAGAT 1680
 DB 1670 GCAAAAGTGCATTTGTTCAAGGGTTCGTATACACAGATGATTTTATGATGTTGCTAAGAT 1729
 QY 1681 TGAATTCGGTCTCTATTTTGGCTGTTGATCTTTGCTGCAAAAGGGAGAAATTTGGCAAGG 1740

Db 1973 GCATTATCCAGATCTGAAAGGATCCTCATGAAGAACCCAGAGTCTTTTAAAGCAGAA 2032
 QY
 Db 2009 GGCTAAGACCGCAGAGCAACCCCTCCAAAGAAAGATCTTGCCCTCTCTTCCACCCGAA 2068
 Db 2033 GGCTAAGACCGCAGAGCAACCCCTCCAAAGAAAGATCTTGCCCTCTCTTCCACCCGAA 2092
 QY 2069 AGAAGAGACACCCAACTGTTTAAACTCTCTAGAGGCGCAGGAAAGCAAGTCTTGC 2128
 Db 2093 AGAAGAGACACCCAACTGTTTAAACTCTCTAGAGGCGCAGGAAAGCAAGTCTTGC 2152
 QY 2129 AAGACTACTCAAAATGAAAGCGAGCAAGCAGCTCAGAAAGAAAGAAATCTGGAAGGAGG 2188
 Db 2153 AAGACTACTCAAAATGAAAGCGAGCAAGCAGCTCAGAAAGAAAGAAATCTGGAAGGAGG 2212
 QY 2189 AGAAGAGAGGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAAG 2248
 Db 2213 AGAAGAGAGGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAAG 2272
 QY 2249 AATGAGATTAAGAAAGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAG 2308
 Db 2273 AATGAGATTAAGAAAGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAG 2332
 QY 2309 GCCACTGGACAGACCTGAATGTACAGCAAGTCTTATTCAGTGGAGGAGAAACCCCACTC 2368
 Db 2333 GCCACTGGACAGACCTGAATGTACAGCAAGTCTTATTCAGTGGAGGAGAAACCCCACTC 2392
 QY 2369 AGTTAGAGGACAGTTTACCCAGAGGAGCTCTCGTCAATCACTCATATCAGCATGGC 2428
 Db 2393 AGTTAGAGGACAGTTTACCCAGAGGAGCTCTCGTCAATCACTCATATCAGCATGGC 2452
 QY 2429 TCCCTCTGCTGAGGCGGAGAGAGGTTCTTACTATTGAAGTCAAGAAAGAGGCTAAGCA 2488
 Db 2453 TCCCTCTGCTGAGGCGGAGAGAGGTTCTTACTATTGAAGTCAAGAAAGAGGCTAAGCA 2512
 QY 2489 ATAA 2492
 Db 2513 ATAA 2516

RESULT 3
 ABZ80565
 ID ABZ80565 standard; cDNA; 2607 BP.
 AC ABZ80565;
 XX
 XX 26-JUN-2003 (first entry)
 DT
 DE Nucleotide sequence of hbeta1b.
 XX
 XX OCNC1; OCNC2; beta1b; human;
 KW olfactory cyclic nucleotide gated channel subunit; ss.
 XX
 XX Homo sapiens.
 OS
 FN WO2003004611-A2.
 XX
 XX 16-JAN-2003.
 PD
 XX 08-JUL-2002; 2002WO-US021184.
 PF
 XX 06-JUL-2001; 2001US-0303140P.
 PR 10-DEC-2001; 2001US-0337154P.
 XX
 XX (SENO-) SENOMYX INC.
 PA
 XX Zoller MT, Xu H, Staszewski L, Moyer B, Pronin A, Adler JB;
 PI Servant G, Callamaras N;
 PI
 XX WPI; 2003-229406/22.
 DR P-FSDB; ABR39396.
 XX
 PT Novel isolated nucleotide sequences encoding human OCNC1, OCNC2, beta 1b

PT olfactory cyclic nucleotide gated (CNG) channel subunits, useful for
 PT identifying the CNG channel activators useful for enhancing smell.
 XX
 PS Claim 14; Page 89; 97pp; English.
 XX
 CC The present invention relates to a nucleotide sequences encoding human
 CC OCNC1, OCNC2, or beta1b olfactory cyclic nucleotide gated (CNG) channel
 CC subunit, its action being an olfactory CNG channel activity modulator. A
 CC host cell which expresses human OCNC1, OCNC2 and/or beta1b is useful in a
 CC mammalian cell-based assay for the profiling and screening of putative
 CC modulators of a human olfactory cyclic nucleotide gated (CNG) channel.
 CC The method is used to identify a compound as one which particularly
 CC modulates CNG activity based on a detectable change in fluorescence. The
 CC test cell expresses each of the human OCNC1, human OCNC2 and human beta1b
 CC subunits. A fluorescence plate reader or a voltage imaging plate are used
 CC to monitor changes in fluorescence. The compounds that activate olfactory
 CC CNG channel enhance smell and can be used to make foods more palatable
 CC for individuals with attenuated olfactory function. The present sequence
 CC represents the nucleotide sequence of hOCNC1
 XX
 SQ Sequence 2607 BP; 614 A; 782 C; 719 G; 492 T; 0 U; 0 Other;

Query Match 21.4%; Score 577.4; DB 7; Length 2607;
 Best Local Similarity 64.3%; Pred. No. 2.3e-112;
 Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;
 QY 679 TTCCAAACAGCAGTAGATTTCATACAGACGACTCTATCTCTCTGCTGCTCTGCTGCTCA 738
 Db 782 TTCCCCAGAGCATGACCCGCTGACCACTGATGATGCTCTATGCTGCTCTCTGCTGG 841
 QY 739 CTCTTCCCTATAACTGGAACTGCTGCTTTATACCACTGCGCTCTCTTCCCATATCAA 798
 Db 842 TGAATGCTGGAATGGAACTGTGGTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTCA 901
 QY 799 CCGCAGACAACTATCACTACTGCTTATTCGGACATCATATGATATCATCTACTCTTT 858
 Db 902 CCCCAGACAACTATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
 QY 859 ATGATATGCTATTATTCAGCCAGACCTCCAGCTTTGTAAGAGGAGGAGACATAATAGTGG 918
 Db 962 TGGACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1021
 QY 919 ATTCAATGAGCTAAGGAAACCTACAGACTTCTACAAATTTCAAGATTCAGTTCGAT 978
 Db 1022 ACAAAAAGGACATGCGAAATACTACCTGAACTCTCGCGCTTCAAGATGAGACCTGCTCA 1081
 QY 979 CAATAATACCATTTGATATTTCTGCTACCTCTCTTTGGGTTTAAATCCAATGTTAGAGCA 1038
 Db 1082 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1141
 QY 1039 ATAGGATGTTAAAGTACACTTCATTTTGAATTTAATCATCACCTAGAGTCTATAATGG 1098
 Db 1142 CCGCTGTTTAAAGTACATGCGCTTCTTCGAGTTTAAACAGCGCGCTGGAATCCATCTCA 1201
 QY 1099 ACAAGCATATATCTACAGAGTTATTCGAACACTGGATCTGCTGCTGCTGCTGCTGCTG 1158
 Db 1202 GCAAGCCTACGTTGACAGGGTCAACAGACCAAGCCTTACCTTCTACAGCTGCTGAT 1261
 QY 1159 TTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1218
 Db 1262 TGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1321
 QY 1219 TGTATGATGGGAAGAAACAGATATCTGAGATGTTATTTATTTGGCAGTTCGAATTTAA 1278
 Db 1322 TTTACGATGGCTGGGAAACAGTTATATTCGCTGTTTACTTCTGCTGTTGAGACCTCTCA 1381
 QY 1279 TTACCATTTGGTGGCTTTCAGAACCAACAACTTTATTTGAAATTTTTCCTCAACTCTTGA 1338
 Db 1382 TCACCATCGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1441
 QY 1339 ATTTTCTGAGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1398
 Db 1442 ATTATTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1501

Db 83 GCAACTATCAAGGACAGAAAACCAACACCGCATGTTCTCACACACAGCCACAAA 142
 QY 409 ACAACCGCTGAGCTCTGTTATTAATAGATAGCCGATGCCCCAGCTACACAACTGG 468
 Db 143 ACAACCGCTGAGCTCTGTTATTAATAGATAGCCGATGCCCCAGCTACACAACTGG 202
 QY 469 TGAAGAAGATGGTCAAGAACAGCCCTCTACAGAAAAGTTGGTAGAGGAGATCTCT 528
 Db 203 TGAAGAAGATGGTCAAGAACAGCCCTCTACAGAAAAGTTGGTAGAGGAGATCTCT 262
 QY 529 CCTCACCCGAAGCCAGCCACAAAAGTGAAGAGCCAGCCCTGTACACACAGTAAAGAAA 588
 Db 263 CCTCACCCGAAGCCAGCCACAAAAGTGAAGAGCCAGCCCTGTACACACAGTAAAGAAA 322
 QY 589 GCGATGATGAAGCAACAGAACATTAAGCAAGCTGTTGGTTCAAAGTCAAAAGATGC 648
 Db 323 GCGATGATGAAGCAACAGAACATTAAGCAAGCTGTTGGTTCAAAGTCAAAAGATGC 382
 QY 649 CTTTAAACAGATGACTTAAAGCGAATTAAGTTCAAACAGCATAGATTCATACAGATC 708
 Db 383 CTTTAAACAGATGACTTAAAGCGAATTAAGTTCAAACAGCATAGATTCATACAGATC 442
 QY 709 GACTCTATCTCTGGCTCTGTTGTCATCTTGCCTTAATGATGCTATTATCCAGCCAGCTCC 768
 Db 443 GACTCTATCTCTGGCTCTGTTGTCATCTTGCCTTAATGATGCTATTATCCAGCCAGCTCC 502
 QY 769 TACCACTGGCTCTGTTCCATATCAACCGCAGCAACATACACTGCTGTTATTG 828
 Db 503 TACCACTGGCTCTGTTCCATATCAACCGCAGCAACATACACTGCTGTTATTG 562
 QY 829 CGGACATCATATGATATCATCTACCTTTATGATGCTATTATCCAGCCAGCTCC 888
 Db 563 CGGACATCATATGATATCATCTACCTTTATGATGCTATTATCCAGCCAGCTCC 622
 QY 889 AGTTGTGAAGGAGGAGACATAATA 914
 Db 623 AGTTGTGAAGGAGGAGACATAATA 648

RESULT 7

AAS76184/c

ID AAS76184 standard; cDNA; 2244 BP.

XX AAS76184;

AC AAS76184;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #11988.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG11997.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX Claim 1; SEQ ID NO 11988; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 2244 BP; 463 A; 592 C; 469 G; 720 T; 0 U; 0 Other;

Query Match 19.2%; Score 518; DB 5; Length 2244;
 Best Local Similarity 94.7%; Pred. No. 8.5e-100;

Matches 536; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 349 GAACAGTCCAGCAGCAGAGGAAATGGACCCCGGAAAGAGGTCCAAACAGCCACAAA 408

Db 2162 GCAAACTATCAAGGACAGAAAACCAACACCGCATGTTCTCACACACAGCCACAAA 2103

QY 409 ACAACCGCTGAGCTCTGTTATTAATAGATAGCCGATGCCCCAGCTACACAACTGG 468

Db 2102 ACAACCGCTGAGCTCTGTTATTAATAGATAGCCGATGCCCCAGCTACACAACTGG 2043

QY 469 TGAAGAAGATGGTCAAGAACAGCCCTCTACAGAAAAGTTGGTAGAGGAGATCTCT 528

Db 2042 TGAAGAAGATGGTCAAGAACAGCCCTCTACAGAAAAGTTGGTAGAGGAGATCTCT 1983

QY 529 CCTCACCCGAAGCCAGCCACAAAAGTGAAGAGCCAGCCCTGTACACACAGTAAAGAAA 588

Db 1982 CCTCACCCGAAGCCAGCCACAAAAGTGAAGAGCCAGCCCTGTACACACAGTAAAGAAA 1923

QY 589 GCGATGATGAAGCAACAGAACATTAAGCAAGCTGTTGGTTCAAAGTCAAAAGATGC 648

Db 1922 GCGATGATGAAGCAACAGAACATTAAGCAAGCTGTTGGTTCAAAGTCAAAAGATGC 1863

QY 649 CTTTAAACAGATGACTTAAAGCGAATTAAGTTCAAACAGCATAGATTCATACAGATC 708

Db 1862 CTTTAAACAGATGACTTAAAGCGAATTAAGTTCAAACAGCATAGATTCATACAGATC 1803

QY 709 GACTCTATCTCTGGCTCTGTTGTCATCTTGCCTATAACTGGAACCTGCTGTTTA 768

Db 1802 GACTCTATCTCTGGCTCTGTTGTCATCTTGCCTATAACTGGAACCTGCTGTTTA 1743

QY 769 TACCACTGGCTCTGTTCCCATATCAACCGCAGACACATACACTGCTGTTATTG 828

Db 1742 TACCACTGGCTCTGTTCCCATATCAACCGCAGACACATACACTGCTGTTATTG 1693

QY 829 CGGACATCATATGATATCATCTACCTTTATGATGCTATTATCCAGCCAGACTCC 888

Db 1692 CGGACATCATATGATATCATCTACCTTTATGATGCTATTATCCAGCCAGACTCC 1623

QY 889 AGTTGTGAAGGAGGAGACATAATA 914

Db 1622 AGTTGTGAAGGAGGAGACATAATA 1597

AC ADD93243;
 XX DT 29-JAN-2004 (first entry)
 XX DE Cyclic nucleotide gated channel alpha 1 coding sequence.
 XX KW ss; gene; Cyclic nucleotide gated channel alpha 1;
 KW central nervous system; CNS; eye; blood-brain barrier;
 KW blood-retina barrier; angiogenesis; revascularisation;
 KW retinal pigment epithelium; RPE; neurosensory retina; choroidea;
 KW age-related macular degeneration; AMD; diabetic retinopathy;
 KW Alzheimer's disease; Parkinson's disease; depression; bipolar disorder;
 KW schizophrenia; amnesia; headache; stroke; insomnia; alcohol abuse;
 KW anxiety; chronic pain; retinal blastoma; primary retinal detachment.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT 25..2097
 XX FT CDS /tag= a
 XX FT /product= "Cyclic nucleotide gated channel alpha 1"
 XX PN W02003087368-A2.
 XX PD 23-OCT-2003.
 XX PF 16-APR-2003; 2003WO-EP004003.
 XX PR 18-APR-2002; 2002EP-00008761.
 XX PR 05-DEC-2002; 2002US-0431173P.
 XX PA (LYNK-) LYNKEUS BIO TECH GMBH.
 XX PI Drumm K, Schloer SH, Goehring F;
 XX DR P-PSDB; ADD93244.
 XX PT Treating central nervous system and/or eye disorders comprises
 PT administering to a subject a composition comprising a compound that
 PT modulates a target gene or gene product, outside the blood-brain and/or
 PT blood-retina barriers.
 XX PS Claim 19; SEQ ID NO 1; 91pp; English.
 CC This sequence encodes the human cyclic nucleotide gated channel alpha 1
 CC protein. This cDNA may be targeted in the method of the invention for
 CC treating a disorder of the central nervous system (CNS) and/or the eye.
 CC The method comprises administering to a subject a composition comprising
 CC a compound capable of modulating a target gene or gene product in a
 CC therapeutic amount, where the composition is administered outside the
 CC blood-brain and/or the blood-retina barriers. The composition is in a
 CC designed form to be introduced into the cells or tissue of the CNS or eye
 CC by a suitable carrier, characterized by the application occurring outside
 CC the blood-brain or blood-retina barriers. It is also designed for
 CC systemic administration or for administration by iontophoresis, or for
 CC reticular application or as eye drops. The compound, nucleic acid
 CC molecule or vector is useful for the preparation of a composition for
 CC treating, preventing and/or delaying a disorder of the CNS and/or the
 CC eye, e.g. related to angiogenesis and/or neovascularisation, retinal
 CC pigment epithelium (RPE), neurosensory retina and/or choroidea and wet
 CC age-related macular degeneration (AMD) or diabetic retinopathy. The
 CC compound may also be used as a lead compound in drug discovery and
 CC preparation of drugs or prodrugs. The nucleic acid molecule and
 CC polypeptide are also used for the validation of test substances, lead
 CC compounds, drugs and prodrugs for the treatment of the disorder mentioned
 CC above or for the identification and isolation of downstream genes, which
 CC respond to modulation of a gene comprising the nucleic acid molecule, or
 CC its encoded gene product. The method is used for diagnosing, preventing
 CC or treating the disorder cited above, which may include Alzheimer's
 CC disease, Parkinson's disease, depression, bipolar disorder,
 CC schizophrenia, amnesia, headache, stroke, insomnia, alcohol abuse,
 CC anxiety, chronic pain, retinal blastoma, primary retinal detachment or

CC age-related macular degeneration.
 XX Sequence 2500 BP; 861 A; 431 C; 525 G; 683 T; 0 U; 0 Other;
 SQ
 Query Match 6.5%; Score 176.4; DB 9; Length 2500;
 Best Local Similarity 49.6%; Pred. No. 2.1e-27;
 Matches 617; Conservative 0; Mismatches 591; Indels 36; Gaps 5;
 QY 802 CAGACACATACACTACTGCGCTATTTGCGGACATCATATGTGATATCATCTACCTTTATG 861
 DB |||||
 QY 605 CTGATTACCTAGAAATATTTGGCTCATTTTGGATTAAGTATCAGACATAGTCTATTTAATCG 664
 DB |||||
 QY 862 ATATGCTATTTATCCAGCCGACACTCCAGTTTGTATAGAGGAGGACAGACATAAATAGTGGATT 921
 DB |||||
 QY 665 ATATG---TTTGACGAACAAGGACAGGTTACCTAGNACAAGGACGCTGCTGTAAGGAAG 721
 DB |||||
 QY 922 CAATGAGCTAGGAAACACTACAGGACTTCTACAAAATTTTCAGTTGGATGTCGATCAA 981
 DB |||||
 QY 722 AACTTAACTCATATAATAATAATAATCCAACTTGCATTTTAACTTGTATGTTCTGTGAC 781
 DB |||||
 QY 982 TAATACCATTTGATATTTGCTACCTCTCTCTTTGGGTTTA---ATCCAATGTTTAGAGCA 1038
 DB |||||
 QY 782 TGNATCAACTGATTTGCTGATTTTAAGTTAGGTGGAACTATCCAGAAATAGATTAA 841
 DB |||||
 QY 1039 ATAGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCACCCTAGAGTCTATAATGG 1098
 DB |||||
 QY 842 ACAGGTTGTTAGGTTCTCTCGTATGTTTGTAGTTCTCCAGAGAACAGAAACAAGGACAA 901
 DB |||||
 QY 1099 ACAAGCATATATCTACAGAGTTATTCGACAACTGGATCTTGTCTGTTTATTTCTGACA 1158
 DB |||||
 QY 902 ACTATCCAAACATCTTCAGAACTTCCAACTTGTGTTATGTATATGTCATCATTTATCCACT 961
 DB |||||
 QY 1159 TTAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGG 1218
 DB |||||
 QY 962 GGAATGCAATGTTGTTCTACTCTATTTCTAAAGCTATTGGATTGGAATGATATACATGG 1021
 DB |||||
 QY 1219 TGTA-----TGATGGGAAGGAACAGAGTATCTGAGATGTT 1254
 DB |||||
 QY 1022 TCTACCTGATATTAATGATCTGAATTTGGCGGTTTGGCTAGAAATACGTATACAGCC 1081
 DB |||||
 QY 1255 ATTATTGGGCACTTCCAACTTTAATTACATTTGGTGCGCTTCCAGAACCAAACTTTAT 1314
 DB |||||
 QY 1082 TTTACTGGTCTACACTGACTTTGACTACCATTTGGTGAACACCCCTCCGCTAGGAGTT 1141
 DB |||||
 QY 1315 TTGAAATGTTTTCACACTCTTGAATTTTCTGGAGTTTGTGTTTCTCCAGTTTAA 1374
 DB |||||
 QY 1142 CTGAGTATGTTCTTTGTTGGTGGTGTATTTCTTAATTTGGAGTGTAAATTTTGTCTACCATCG 1201
 DB |||||
 QY 1375 TTGGTTCAGATGAGAGATGTTGAGGAGCTACAGCCCAATCAGAACTACTTCCGCGCT 1434
 DB |||||
 QY 1202 TTGGTAAATAGGTTCTATGATTTCCAACTGAATGAGCCAGAGCAGAAATTTCAAGCAA 1261
 DB |||||
 QY 1435 GATGATGACACCACTTCCCTACATGAACAAATTAATCTCCATTTCTTAACTTTGTGCAAAAGC 1494
 DB |||||
 QY 1262 GAATTTGATGCTATCAAGCAATATATGCAATTTTCCAAATGTAAGCAAGATATGCAAAAGA 1321
 DB |||||
 QY 1495 GAGTTTCGAGCTTGGTATGCAATATACATGGGACTCTCAAGAACTCTAGATGAGTCTGATT 1554
 DB |||||
 QY 1322 GGGTTATTAAATGGTTTACTACCTGTGGACCAACAAAACAAAGTGTGATGAGAAAG 1381
 DB |||||
 QY 1555 TGCTTAAGACCTTACCACTACGCTCCAGTTTAGCCCTCGCCATTTGATGTGAATTTACGCA 1614
 DB |||||
 QY 1382 TCTTAAAGTATCTACCTGATATAACTAAGAGCAGAAATTTGCCATCAACGTTCACTTACACA 1441
 DB |||||
 QY 1615 TCATCAGCAAGTTCGACTTGTTCAGGGTTGTGATACAGATCATTTATGACATGTTC 1674
 DB |||||
 QY 1442 CATTAAGAAAGGTACGCACTTTTCTGATTTGAGTGTGTTCTGTTGGTGGATGTTGCT 1501
 DB |||||
 QY 1675 TAAGATTGAAATCCGTTCTCTTATTTGCTGGTGTACTTTGTCTGCAAAAGGAGAAATTTG 1734
 DB |||||
 QY 1502 TGAATTCGAACCCCAAGTCTTACAGTCTCTGAGATTATATTGCAAGAAAGGGGATATCG 1561
 DB |||||
 QY 1735 GCAAGGAATGATATATCATCAAGCATGAGAACTCCAAAGTCTTGGAGGCCCTGATGGTA 1794

XX Identifying a compound for treating urological disorders, for example
PT urinary incontinence by assaying the ability of the compound to modulate
PT the nucleic acid expression or polypeptide activity.
XX
PS Disclosure; Page 156-159; Opp; English.
XX
XX The present relates to a method for identifying a compound for treating
CC urological disorders e.g., urinary incontinence including overactive/
CC overactive bladder, overflow urinary incontinence, stress urinary
CC incontinence caused by dysfunction of the bladder, urethra or central
CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,
CC cancer of the prostate or kidney disorders. The method is also useful, for
CC modulating hyperplasia in a cell and treating a subject having a
CC urological disorder. The invention is also used in gene therapy. The
CC present sequence is human CNG channel alpha 3 potassium channel (KCNO2)
CC DNA
XX
SQ Sequence 3486 BP; 912 A; 866 C; 865 G; 843 T; 0 U; 0 Other;
Query Match 4.9%; Score 132.8; DB 9; Length 3486;
Best Local Similarity 49.2%; Pred. No. 3.9e-18;
Matches 487; Conservative 0; Mismatches 472; Indels 31; Gaps 4;
QY 918 GATTCATAGCTAAGCAACACTACAGGACTCTACAAATTCAGTTGGATGCGCA 977
Db 742 GATACCAACAGGCTGTGCGACATTAACAGACGACCGAGTTCAGCTGGATGTTG 801
QY 978 TCAATAATACATTGATATTGCTACTCTCTCTTTGGTTTAA---ATCAATGTTTGA 1034
Db 802 TCCCTGGTCCCGACCGCTGCTTAAAGTGGGCAAACTACCCAGAAGTAGG 861
QY 1035 GCAATAGGATGTTAAAGTACACTTCTTTTGAATTTAATCATCACTAGTCTATA 1094
Db 862 TTCAACCGCTTACTGAAGTTTTCGGCTCTTTGAATTTCTTGACCGCACAGACAAG 921
QY 1095 ATGACAAAGCATATATACAGAGTTATTTCGAACAATCGATCTGCTTTATTCGT 1154
Db 922 ACCAATACCCCATATGTTCCGATTTGGGAATCTGTTGATCATCATCATC 981
QY 1155 CACATTAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGAAATGGCACTACTA 1214
Db 982 CACTGGATGCTGCTACTCTTTGCCATTTCCAAAGTTTCAATGTTTGGGACAGACTC 1041
QY 1215 TGGTGT-----ATGATGGGAAGGAACGATCTCTGAGA 1250
Db 1042 TGGGTCTACCAAAATCATCAATCCAGAGATGGGCGCTCTCCAGAGATCATTTAC 1101
QY 1251 TGTATTATTGGGAGTTTGAACCTTAAATACCATTTGTTGGCTTCCAGAACCAAACT 1310
Db 1102 AGTCTCTACTGCTCACCTTGACCTTACCACCATTTGGTGAGACCCACCCCGTGAAA 1161
QY 1311 TTATTGAAATGTTTTCCTTGAATTTTCTGAGTTTCTGAGTTTCTGCTTCCAGT 1370
Db 1162 GATGAGGAGTATCTCTTTGCTGCTAGACTTCTTGGTGGTGTCTGATTTTGGCCACC 1221
QY 1371 TTAATTGTCAGATCAGAGATGTTGATTTGGAGCAGCTACAGCAATTCAGAACTACTCCG 1430
Db 1222 ATTTGGGCAATGCGGCTCCATGATCTCGATATGAATGCTCAGCGGAGAGTTCCAG 1281
QY 1431 GCTGTCATGATPACACCATTCCTTACATGAACAAATTAATCTCCATTCCTTAACTTTGCAA 1490
Db 1282 GCCAAGATGATTCCATCAAGCAGTACATGCTAGTTTCCGCAAGGTCCCAAGGACTTGGAG 1341
QY 1491 AAGCAGATTCGACTTGGTATGAATATACATGGGACTCTCAAGAAATCTAGATGAGTCT 1550
Db 1342 ACGCGGTTATCCGGTGGTTTGAATCTCTGCGGCAACAGAACGCGTGGATGAGAAG 1401
QY 1551 GATTTGCTTAAGACCCCTACCAACTACGGTCCAGTTAGCCCTCGCATGATGTAACATTC 1610
Db 1402 GAGTGTCTAAGAGCTCTCCAGACAGCTGAAGGCTGAGATCGCATCAACGTCACCTG 1461
QY 1611 AGCATCATCAGCAAGTACTTGTTCAGGGTGTGTGATACACAGATGATTTATCATG 1670

Db 1462 GACACGCTGAAGAAGTTCCGATCTTCAGGACTGTGAGGAGGCTGCTGGTGGAGCTG 1521
QY 1671 TTGCTAAGATTGAATCGTTCTCTATTGCTCGTACTTTGCTGCTGCTGCTGCTGCTGCTG 1730
Db 1522 GTGCTGAAGCTGCGACCCACTGTGTTGAGCCCTGGGATTATATCTGCAAGAGGAGAT 1581
QY 1731 ATTGCAAGGAATCTATATCATCAAGCATGAGAGTCCAAAGTTCTTGGAGGCCCTGAT 1790
Db 1582 ATTGGAAGGAGATGATCATCATCAACAGAGGCAAGCTGGCCGTGGTGTGATGATGGG 1641
QY 1791 GGTACTAAAGTTCTGGTTACTCTCTCAAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1849
Db 1642 GTACCCAGTTCGTTGTT---CTCAGCGATGCGAGCTACTTCCGGGAGATCAGCATTCG 1698
QY 1850 AGCAGCAGAGAGAGAAACCGTCGAACTGC 1879
Db 1699 AACATCAAGGAGCAAGTCGGGGAACCGC 1728
RESULT 13
AAD56241
ID AAD56241 standard; DNA; 1995 BP.
XX
AC AAD56241;
XX
DT 07-AUG-2003 (first entry)
XX
DE Rat CNG channel alpha subunit mutant DNA #2.
XX
KW Rat; G protein-coupled receptor; cyclic nucleotide-gated channel; GPCR;
KW cyclic nucleotide-gated channel; CNG channel; mutant; gene; ds.
XX
OS Rattus norvegicus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..1995
FT /tag= a
FT /product= "CNG channel alpha subunit mutant protein"
XX
PN WO2003038039-A2.
XX
PD 08-MAY-2003.
XX
PF 25-OCT-2002; 2002WO-US034122.
XX
PR 26-OCT-2001; 2001US-0330663P.
PR 04-MAR-2002; 2002US-00087217.
XX
PA (APTU-) APTUS PHARM INC.
XX
PI Yao Y, Cao L;
XX
XX WPI; 2003-430510/40.
DR P-PSDB; AAE37221.
XX
XX New host cell comprising first and second nucleic acids with promoters
XX that encode exogenous G protein-coupled receptor and cyclic nucleotide-
XX gated channel, respectively, useful for identifying agents that modulate
XX GPCR activity.
XX
XX Claim 12; Page 86-89; 98pp; English.
XX
XX The invention relates to compositions and methods for identifying G
XX protein-coupled receptor (GPCR), ligands and compounds that modulate GPCR
XX mediated activities. The invention also provides an host cell comprising
XX first and second nucleic acids with promoters that encode exogenous G
XX protein-coupled receptor and cyclic nucleotide-gated (CNG) channel
XX respectively. The host cells are useful for identifying agents that
XX modulate an activity mediated by a GPCR. The present sequence is rat CNG
XX channel alpha subunit mutant encoding DNA

CC	protein-coupled receptor and cyclic nucleotide-gated (CNG) channel respectively. The host cells are useful for identifying agents that modulate an activity mediated by a GPCR. The present sequence is rat CNG channel alpha subunit wild-type DNA	XX
CC	Sequence 1995 BP; 529 A; 460 C; 505 G; 501 T; 0 U; 0 Other;	
QY	Query Match 4.9%; Score 131.6; DB 7; Length 1995;	
QY	Best Local Similarity 46.7%; Pred. No. 6e-18;	
QY	Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;	
QY	714 TATCTCTCTGGCTCTTGGCTGTGTCATCTTTCCTATTAACGTGGAACCTGCTGGTTTATACCA 773	
DB	424 TATTACCGTTGGTTTGTGTCATTGCGCATGCCCTGTCTTTTACAACTGGTGCCTGTGTGGTG 483	
QY	774 CTGGCGCTGCTCTTCCCATATCAAAACGGAGACAACATACACTACTACTGGCTTATTCGGGAC 833	
DB	484 GCCAGAGCCCTTCAGTGTATCTACAGAGAAACTATTTTGTGGTATGGCTGGTCTGGAG 543	
QY	834 ATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCCAAGATCCACAGTTT 893	
DB	544 TACTTCTCAGACACTGTCTATATCGCAGACCTCATCTTCGGCTGCGCACAGGC---TTC 600	
QY	894 GTAAGAGGAGGACATATAATAGTGGATTAAGATGAGCTAAGAGAAACACTACAGGACTTCT 953	
DB	601 CTGAACAGGGGCTCTTGGTCAAGAAGATCCCAAGAAATGCGAGACAACATATATTCACACT 660	
QY	954 ACAAAATTTTCAGTTGGATGTCGATCAATAATACCAATTTGATATTTGCTACCTCTCTCTT 1013	
DB	661 TTGCAGTTCAAAATGGATGTCGCTTCTATCATTTCCCACTGACCTTATCTATTTTGGCTGTG 720	
QY	1014 GGGTT---TAATCCAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCATTTTTTGGAA 1070	
DB	721 GGTATCCACAGCCCTGAGGTACGCTCAACCGCTCTATTACACTTGCCTGATGTTTGGAG 780	
QY	1071 TTTAATCATCACCTAGAGTCTATAATGGACAAGACATATATCTACAGAGTTATTCGAACA 1130	
DB	781 TTCTTTACCGCACTGAGACAGCAGCACTACCCCAACATCTTCCGAATCAACAATCTG 840	
QY	1131 ACTGGATACTTGCCTTTATTCTGCACATTAATGCGCTGTGTTTATTACTGGGCTTCAAAC 1190	
DB	841 GTCCTTTACATCTTGGTCAATCCACTGGAAATGCTTGTATTATTATGTTATTCTAAG 900	
QY	1191 TATGAAGGAATTTGG-----CACTACTAGATGGGTGTATGAT 1226	
DB	901 TCCATTGGCTTTGGAGTTGACACCTGGGTTTACCCCAACATTAAGTACCTGGAATATGGC 960	
QY	1227 GGGGAGGAACAGATATCTGAGATGTTATTATTGGCAGTTCCAACTTTAAATTAACCAT 1286	
DB	961 TACCTGGCTAGAGATGATTTATCTGCTTTACTGGTCCACACTGACCTCACCAACCAT 1020	
QY	1287 GGTGGCCTTCAGAACCCACAACATTTATTGAAATGTTTTTCAACTCTTGAATTTTTTT 1346	
DB	1021 GGAGAGACACCACCCCTGTAAAGGATGAGGAGTACCTATTGTTCATCTTTGACTTCTTG 1080	
QY	1347 TCTGGAGTTTTTGTGTTCTCCAGTTTAAATTCGTTCAGATGAGAGATGTTGGAGCAGCT 1406	
DB	1081 ATTGGTGTCTCATCTTTGCCACTATTGTGGGAATGTGGGCTCCATGATCTCCAAATG 1140	
QY	1407 ACAGCCAATCAGAACTACTTCGGCGCTGCAATGGATGACCACTATGGCTCATGAAACAAT 1466	
DB	1141 AATGCCACAGCAGCAGATTCAGGCCAAGATTGATGCTGTCAAACTACATGACAGTTC 1200	
QY	1467 TACTCCATCTCTAACTTGTGCAAAAGCGAGTTCCGAGCTTGGATGATGATATACATGGAC 1526	
DB	1201 CGAAAGGTCAGCAAGACATGGAAGCCAAAGTTCATCAAAATGGTTTGACTTCTTGTGACC 1260	
QY	1527 TCTCAAGAATGCTAGATGAGTCTGATTTGCTTAAAGACCTTACCACCTACGGTCCAGTTA 1586	
DB	1261 AATAGAGACAGTAGATGAACGAGAGTCTCTCAAGACCTTCCAGCAAAAGCTCAGGCT 1320	
QY	1587 GCCCTCGCAATGTATGTGAACTTTCAGATCATCAGCAAGTCGACTGTTTCAAGGTTGT 1646	

CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 526 BP; 174 A; 119 C; 99 G; 134 T; 0 U; 0 Other;

Query Match 4.8%; Score 129; DB 4; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	272	AGACAACTCTCCAAAGAAAAATTCCTCTGGAGATCTGACCAACACCCCTGACCCCTCAAAA	331
Db	191	AGACAACTCTCCAAAGAAAAATTCCTCTGGAGATCTGACCAACACCCCTGACCCCTCAAAA	250
QY	332	TGCACGAGAACCACTGGAACAGTCCACAGACGAGAGAAATGGACCCCGGGAAGAAGG	391
Db	251	TGCACGAGAACCACTGGAACAGTCCACAGACGAGAGAAATGGACCCCGGGAAGAAGG	310
QY	392	TCCAAACAG	400
Db	311	TCCAAACAG	319

Search completed: June 21, 2004, 19:01:03
Job time : 1020.37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 18:18:50 ; Search time 6748.81 Seconds
(without alignments)
11960.251 Million cell updates/sec

Title: US-09-855-828-2

Perfect score: 2703
Sequence: 1 cattctctacctaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthm:*

3: em_estin:*

4: em_estov:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_estc:*

12: gb_estd:*

13: gb_este:*

14: gb_estf:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vit:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	886.2	32.8	2056	11 AK040140	AK040140 Mus muscu
2	553	20.5	553	10 BF725470	BF725470 bx16c03.y
3	526	19.5	527	9 AL713036	AL713036 DXFZP686A
4	470	17.4	655	10 BB635459	BB635459 BB635459

C	5	430.2	15.9	437	10	BF725459
	6	402.4	14.9	881	10	BE287002
	7	363.8	13.5	1201	13	EX401127
	8	328.4	12.1	832	12	B1827605
	9	320.8	11.9	468	9	AA069559
	10	317	11.7	445	14	H53423
	11	308.4	11.4	978	13	BQ68992
	12	301.4	11.2	694	9	AU137778
	13	285.8	10.6	741	13	BX104558
	14	280.8	10.4	738	12	B1736222
	15	280.4	10.4	758	9	AV726367
	16	280	10.4	423	12	BM938767
	17	271.2	10.0	545	10	AA465556
	18	262.2	9.7	563	12	BG304577
	19	261.6	9.7	503	9	AI150392
	20	245.6	9.1	674	29	CC498739
	21	234	8.7	247	9	AA317961
	22	232.4	8.6	270	9	AA012972
	23	224	8.3	325	10	BE982488
	24	219	8.1	696	13	BW269181
	25	216.2	8.0	518	9	AV605886
	26	216.2	8.0	747	12	B1733974
	27	212.4	7.9	215	9	AA069498
	28	211	7.8	869	14	CD327412
	29	201.6	7.5	993	13	BX370500
	30	197.2	7.3	581	9	AV605887
	31	165.6	6.1	353	9	AL120448
	32	164	6.1	376	9	AL120239
	33	131.2	4.9	591	29	CC571022
	34	129.8	4.8	573	12	BM354832
	35	120.6	4.5	535	9	AL928461
	36	111	4.1	920	13	BUI139545
	37	110.6	4.1	490	13	BQ639921
	38	109.2	4.0	584	12	BM862371
	39	106.8	4.0	819	13	BU287884
	40	105.6	3.9	1215	28	CC245670
	41	102.8	3.8	795	13	BU291723
	42	97.6	3.6	573	29	CG985260
	43	96.6	3.6	706	9	AJ442203
	44	94.4	3.5	800	29	CNS03HXC
	45	92.2	3.4	567	10	BF937274

ALIGNMENTS

RESULT 1
AK040140
LOCUS AK040140
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone: A430069G05 product: cyclic nucleotide gated channel beta 3, full insert sequence.
ACCESSION AK040140
VERSION AK040140.1 GI:26087649
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 9279253
PubMed 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PubMed 11042159

AK040140 2056 bp mRNA linear HTC 19-SEP-2003
Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone: A430069G05 product: cyclic nucleotide gated channel beta 3, full insert sequence.

AK040140

AK040140.1 GI:26087649

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

9279253

10349636

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	Matches 1154; Conservative 0; Mismatches 288; Indels 55; Gaps 4;
TITLE		RIKEN Integrated Sequence Analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer	
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)	
MEDLINE		20530913	
PUBMED		11076861	
REFERENCE	4		
AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
TITLE		Functional annotation of a full-length mouse cDNA collection	
JOURNAL		Nature 409, 685-690 (2001)	
REFERENCE	5		
AUTHORS		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
TITLE		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
JOURNAL		Nature 420, 563-573 (2002)	
REFERENCE	6	(bases 1 to 2056)	
AUTHORS		Adachi, J., Aizawa, K., Akimura, T., Avakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, Y., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
TITLE		Direct Submission	
JOURNAL		Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
COMMENT		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
FEATURES		Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://phantom.gsc.riken.go.jp/ Location/Qualifiers	
source		1..2056 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:A430069G05" /db_xref="MGI:2404764" /db_xref="taxon:10090" /clone="A430069G05" /tissue_type="thymus" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="0 day neonate"	
misc_feature		1..2056 /notes="cyclic nucleotide gated channel beta 3 (MGD MGI:1353562, GB NM_013927, evidence: BLASTN, 100%, match=2055)"	
ORIGIN			
Query Match		32.8%; Score 886.2; DB 11; Length 2056;	
Best Local Similarity		77.1%; Pred. No. 3.2e-134;	

QY 2218 AACAAAGAAATAGAGATTAACAAAGAAATGAAGTAAAGAAAGAAATGAAG 2277
 DB 1044 GTTCCAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
 QY 2278 ATAAAGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2337
 DB 1104 AAAAGAAGA-----AAAAGAACCCAGTGGATAGTTCAGAGGACACTAA 1149
 QY 2338 GTTCCTATTCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2397
 DB 1150 GTTCCTATTCAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1209
 QY 2398 CTTCTCGTCAATCACTCAATCACTCACTCACTCACTCACTCACTCACTCA 2457
 DB 1210 ATGCGCTATCAATTCATCAGCAACATGG-TCCGTCTACTGAGACTGGAGAGAGATTC 1268
 QY 2458 TTACTATTGAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2517
 DB 1269 TCACTATCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1328
 QY 2518 ATAGCTAGTTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2577
 DB 1329 CTAGCTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1386
 QY 2578 ACATGCTGGAGCCCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2634
 DB 1387 ACCTCACTGGAGCCCTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443
 RESULT 2
 BF725470 553 bp mRNA linear EST 05-JAN-2001
 LOCUS bxi6c03.y1 Human Iris cDNA (Un-normalized, unamplified): BX Homo
 DEFINITION sapiens cDNA clone bxi6c03 5', mRNA sequence.
 ACCESSION BF725470
 VERSION BF725470.1 GI:12041381
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 553)
 Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
 NEIBANK: EST analysis and bioinformatics for ocular genomics
 Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
 Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 16 row: c column: 03
 Seq primer: M13Rpl reverse primer (ABI).
 Location/Qualifiers
 1..553
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="bxi6c03"
 /tissue_type="Iris"
 /dev_stage="Adult"
 /lab_host="EMBL10B"
 /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
 BX"

FEATURES

source

RESULT 3
 AL713036
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 527)
 Bloecker,H., Boecker,M., Brandt,P., Mewes,W., Weill,B. and
 Wiemann,S.
 EST (Bloecker,H., Boecker,M., Brandt,P., Mewes,H.W., Weill,B. and
 Wiemann,S.)
 JOURNAL
 Unpublished (1999)

AL713036 527 bp mRNA linear EST 04-SEP-2003
 DKEZP686A1695.r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 DKEZP686A1695 5', mRNA sequence.
 AL713036
 AL713036.1 GI:19696392
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 527)
 Bloecker,H., Boecker,M., Brandt,P., Mewes,W., Weill,B. and
 Wiemann,S.
 EST (Bloecker,H., Boecker,M., Brandt,P., Mewes,H.W., Weill,B. and
 Wiemann,S.)
 JOURNAL
 Unpublished (1999)

full details of which are contained in the manufacturer's
 instruction manual (http://www.lifetech.com/). First
 strand synthesis was carried out using a Not I
 primer-adaptor
 [5'-pGACTAGTTCCTAGATCCGAGCGGCGCCCT(7)15-3']. Not I/blunt
 end inserts were cloned into the Not I/EcoR V sites in the
 vector. EST analysis was performed on the unamplified
 library at the NIH Intramural Sequencing Center (NISC).

ORIGIN

Query Match 20.5%; Score 553; DB 10; Length 553;
 Best Local Similarity 100.0%; Pred. No. 6e-80;
 Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1145 GTTATTCTGCACATTAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTGG 1204
 DB 1 GTTATTCTGCACATTAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTGG 60
 QY 1205 CACTACTAGATGGGTGATGATGGGGAAGAAACAGATATCTGAGATGTTATTATTGGGC 1264
 DB 61 CACTACTAGATGGGTGATGATGGGGAAGAAACAGATATCTGAGATGTTATTATTGGGC 120
 QY 1265 AGTTCGAACCTTTAATTACCATTTGGCTTCCAGAACCAAACTTTATTGAAATTGT 1324
 DB 121 AGTTCGAACCTTTAATTACCATTTGGCTTCCAGAACCAAACTTTATTGAAATTGT 180
 QY 1325 TTTTCAACTCTGTAATTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAATTGGTCAGAT 1384
 DB 181 TTTTCAACTCTGTAATTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAATTGGTCAGAT 240
 QY 1385 GAGAGATGTTGAGGAGCTACAGCAATTCAGAACTACTTCCGCCCTGCATGGATGA 1444
 DB 241 GAGAGATGTTGAGGAGCTACAGCAATTCAGAACTACTTCCGCCCTGCATGGATGA 300
 QY 1445 CACCATTCCCTACATGAACAATTAATCTCCATTCTTAAACTTTGTGCAAAAGCGAGTTCGGAC 1504
 DB 301 CACCATTCCCTACATGAACAATTAATCTCCATTCTTAAACTTTGTGCAAAAGCGAGTTCGGAC 360
 QY 1505 TTGGTATGAATATACATGGGACTCTCAAGAGATCTAGAGAGTCTGATTTGCTTAAAGAC 1564
 DB 361 TTGGTATGAATATACATGGGACTCTCAAGAGATCTAGAGAGTCTGATTTGCTTAAAGAC 420
 QY 1565 CTTACCAACTACGGTCCAGTTAGCCCTCGCCATTGATGTGAATTCAGCATCATCAGCAA 1624
 DB 421 CTTACCAACTACGGTCCAGTTAGCCCTCGCCATTGATGTGAATTCAGCATCATCAGCAA 480
 QY 1625 AGTCGACTTGTCAAGGGTGTGATACACAGATGATTATGACATGTTGCTTAAGATTGAA 1684
 DB 481 AGTCGACTTGTCAAGGGTGTGATACACAGATGATTATGACATGTTGCTTAAGATTGAA 540
 QY 1685 ATCCGTTCTCTAT 1697
 DB 541 ATCCGTTCTCTAT 553

COMMENT

Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.

No sl sequence available.

This clone (DKFZp686A1695) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
1..527
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686A1695"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: sfira; Site_2: sfib;
cDNA-collection"

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 AAGGCACAGTCATAAATACAGAGGTTTTCAGAACCCCTCAGAGAGATGTTTAAATCG 74
Db 2 AAGGCACAGTCATAAATACAGAGGTTTTCAGAACCCCTCAGAGAGATGTTTAAATCG 61
QY 75 CTGCAAAAGTCAACAGGTCAGGCTATAGAGAGACATGATGAACAAAGTTCT 134
Db 62 CTGCAAAAGTCAACAGGTCAGGCTATAGAGAGACATGATGAACAAAGTTCT 121
QY 135 CGTCGAATGAAGAGGCTCTCACCAGTAATCAGTCTCAGCAAAACACAGCACAGGAA 194
Db 122 CGTCGAATGAAGAGGCTCTCACCAGTAATCAGTCTCAGCAAAACACAGCACAGGAA 181
QY 195 GAAACAAAGTGAAGAGAAATCTCTCAAAACCAAGTCACTCAGTCACTGAGAG 254
Db 182 GAAACAAAGTGAAGAGAAATCTCTCAAAACCAAGTCACTCAGTCACTGAGAG 241
QY 255 CCACACACACATACAGACAAACTCTCCAGAAATTCCTCTGAGATCTGACCA 314
Db 242 CCACACACACATACAGACAAACTCTCCAGAAATTCCTCTGAGATCTGACCA 301
QY 315 AACCTGACCTCAAAATGACAGAGAACCACTGGAACAGTGCAGACAGAGGAAATG 374
Db 302 AACCTGACCTCAAAATGACAGAGAACCACTGGAACAGTGCAGACAGAGGAAATG 361
QY 375 GACCCCGGAAGAGTCCAAACAGCCCAACAAACCGCTCGAGCTCTGTATATA 434
Db 362 GACCCCGGAAGAGTCCAAACAGCCCAACAAACCGCTCGAGCTCTGTATATA 421
QY 435 AATGAGTATGCCAGTGCCTCAGTACACAACTGCTGAAAGAAATGCTCAAGAACAGCC 494
Db 422 AATGAGTATGCCAGTGCCTCAGTACACAACTGCTGAAAGAAATGCTCAAGAACAGCC 481
QY 495 CTCTACAGAAAGTGGTAGGGAGATCTCTCTCACCAGG 540
Db 482 CTCTACAGAAAGTGGTAGGGAGATCTCTCTCACCAGG 527

RESULT 4

BB635459

LOCUS

DEFINITION

ACCESSION

BB635459 655 bp mRNA linear EST 26-OCT-2001
BB635459 RIKEN full-length enriched, 0 day neonate thymus Mus
musculus cDNA clone A43069G05 5', mRNA sequence.
BB635459

VERSION
KEYWORDS
SOURCE
ORGANISM

BB635459.1 GI:16471509
EST.
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 655)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Kanagaki, T.,
Konno, H., Kouda, M., Koyu, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ono, M., Okazaki, Y., Okido, T., Saito, K., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sugabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)

TITLE
JOURNAL
COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome.res@gsc.riken.go.jp
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, I.,
Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

e mouse tissues.
Location/Qualifiers
1..655
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A43069G05"
/tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate
thymus"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'-
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 459.0. Second

FEATURES
source

Location/Qualifiers
1..655
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A43069G05"
/tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate
thymus"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'-
GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 459.0. Second

strand cDNA was prepared with the primer adapter of sequence [5' GAGCAGAGATCTCGAGTAATAATATATCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

Query Match 17.4%; Score 470; DB 10; Length 655;
 Best Local Similarity 84.2%; Pred. No. 1.6e-66;
 Matches 553; Conservative 0; Mismatches 101; Indels 3; Gaps 2;

QY	1140	TTGCTGTTTATTCGACATAATAGCTCTGTTGTTTATCTCTGGCTTCAACATCTGAAGGA	1199
DB	1	TTGCTGTTTCTCTCGACATAACGGCTGTGTTTATCTCTGGCTTCAGACTATGAAGGA	60
QY	1200	ATTGGCACTACTAGATGGGTGTATGATGGGAAGGAACGAGATATCTCAGATGTTATATAT	1259
DB	61	ATTGGCTCAACTAAATGGGTCTATAATAGTGAAGGCAACAAGTATCTCGATGCTTTTAT	120
QY	1260	TGGCGAGTTCGAACCTTTAATTACCAANTGGTGGCCITTCAGAACCAACAACCTTATTGAA	1319
DB	121	TGGCGAGTTCGAACCTTTAATTACTATGGGGGGCTTCCAGAGCCACAGACTTCATTTGAA	180
QY	1320	ATTGTTTTTCAACCTCTTGAATTTTTTTTTCTGGAGTTTTTGTCTTCCAGTTTAAATGGT	1379
DB	181	ATTGTTTTTCAATCTTGAATTTTTTCTCTGGGTTTTTGTTTTCTCCAGCTTAAATGGT	240
QY	1380	CAGATGAGAGNTGTGATTTGAGCAGAGCTACAGCCAAATCAGAACTACTTCCGGCCCTGCATG	1439
DB	241	CAGATGGCGTGTGATGTGGGGGAGCAACAGCCAAATCAGAACTACTTCCAAAGCCCTGCATG	300
QY	1440	GATGACACCAATPTGCCTACATGAAACAATTACTCCATTCTTAAACTTGTCCAAAGCGAGTT	1499
DB	301	GACCATATCATTTGCCCTACATGAACAATACTCTATTCTCAGAGTGTCCAGTATCGAGTT	360
QY	1500	CGGACTTGGTATGAATATACATGCGACTCTCAAGAAATCGTAGAGTCTGATTCGCTT	1559
DB	361	CGGACTTGGCTGGGAATATACATGGAATCTCAAGAAGAACTCTAGATGAGTCCAACTTCGCTT	420
QY	1560	AAGACCCCTACCAACTCAGGCTCCAGTTAGCCCTCGCCATTGATGTCAACTTCAGCATCATC	1619
DB	421	GAGAACCTCCGAGCAGCAATGCAATGCTGTCTATTGGCCTTGACATAAACTTCAGTATCATC	480
QY	1620	AGCAAGTCGACTGTTTCAAGGGTGTGTGATACACAGATGATTTATGACATGTTGCTTAAGA	1679
DB	481	GACAAAGTGGAGTTATTCAAGGGCTGTGACACACAGATGATTTATGACCTCTCTCTAAGA	540
QY	1680	TTGAAATCCGTTCTCTATTGTCCTGTTGACTTTGCTCGAAAAAGGGAGAAATGGCAAG	1739
DB	541	TTGAAATCCACTATTATTATTACCTGTTGACTTGTCTGAAAAGGGAGAAATGGCAAG	600
QY	1740	GAAATGTATATCATCAAGCAATGAGAAAGTCCAAAGTTCTTTGGAGGCCCTGTAGTGTACT	1796
DB	601	--AATGTACATCATCAA-CACGAGAAAGTCCAAAGTCTTTGGAGGCCCTGTAGTGTCT	654

[illegible]

Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 495 0078
Email: graeame@helix.nih.gov
Plate: 16 row: c column: 03
Seq primer: -21M13 forward primer (ABI).

FEATURES source

```

1. 437
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="bx16c03"
/tissue_type="iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Iris cDNA (Un-normalized, unamplified):
EX
/notes="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 50ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the SuperScript Plasmid System
full details of which are contained in the manufacturer's
instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACAGTGTTCAGATCGGAGCGGCCGCC(T15-3)'. Not I/blunt
end inserts were cloned into the Not I/ScoR V sites in the
vector. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center (NISC)."

```

ORIGIN

Query Match	15.9%	Score 430.2	DB 10	Length 437
Best Local Similarity	99.3%	Prod. No. 5.4e-60		
Matches 432	Conservative 0	Mismatches 3	Indels 0	Gaps 0
QY	1821	GGGTGGGTGTTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACCTGCC	1880	
DB	437	GGGTGGGTGTTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACCTGCC	378	
QY	1891	AATGTGTGGCCACCGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCCCTCCAGAA	1940	
DB	377	AATGTGTGGCCACCGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCCCTCCAGAA	318	
QY	1941	ATTCTAGTGCATTATCCAGATTCTGAAGGATCCCTCATGAAGAAGCCAGAGTGCCTTTTA	2000	
DB	317	ATTCTAGTGCATTATCCAGATTCTGAAGGATCCCTCATGAAGAAGCCAGAGTGCCTTTTA	258	
QY	2001	AAGCAGAAGGCTAAGACCGCAGAGCAACCCCTCCAGAAAAGATCTTGTGCCCTCCTCTTC	2060	
DB	257	AAGCAGAAGGCTAAGACCGCAGAGCAACCCCTCCAGAAAAGATCTTGTGCCCTCCTCTTC	198	
QY	2061	CCACCGAAAGAGAGACACCCAACTGTGTTTAAAACTCTCTAGAGAGGCACAGGAAAGCA	2120	
DB	197	CCACCGAAAGAGAGACACCCAACTGTGTTTAAAACTCTCTAGAGAGGCACAGGAAAGCA	138	
QY	2121	AGTCTTCCAAAGTACTCAAAATTTGAAGCGAGAGCAGCAGCTCAGAGAAAAGAAATTCCT	2180	
DB	137	AGTCTTCCAAAGTACTCAAAATTTGAAGCGAGAGCAGCAGCTCAGAGAAAAGAAATTCCT	78	
QY	2181	GAAGCGAGAGAGAGAGAGGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAA	2240	
DB	77	GAAGCGAGAGAGAGAGAGGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAA	18	
QY	2241	CAAAAGAAAATGAA	2255	
DB	17	CAAAAAAAAAAAAAA	3	

```

RESULT 6
BE287002 601097229F1 NCI_COAP_Mam5 Mus musculus cDNA clone IMAGE:3496015 5', EST 26-OCT-2000
LOCUS BE287002 881 bp mRNA linear EST 26-OCT-2000
DEFINITION BE287002 mRNA sequence.
ACCESSION BE287002
VERSION BE287002.1 GI:9165707
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM8547 row: i column: 08
High quality sequence stop: 774.
Location/Qualifiers
1. .881
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3496015"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mams"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
ORIGIN
Query Match 14.9%; Score 402.4; DB 10; Length 881;
Best Local Similarity 73.9%; Pred. No. 1.2e-55;
Matches 548; Conservative 0; Mismatches 171; Indels 23; Gaps 2;
QY 1521 TGGAGCTCTCAAGAAATGTAGATGAGTCTGATTTGCTTAAGACCTTACCAACTACGGTC 1580
DB 1 TGGAACTCAAAAGATCTAGATGAGTCCAACTTGTCTGGAACCTCCCGACAGCAATG 60
QY 1581 CAGTTAGCCTCGCCATTCATGTGAACTTCAGCATCATCAGCAAGTCGACTTCTTCAAG 1640
DB 61 CAGTTGCTATTGCTTGCATTAAGAACTTCAGTATCATCGACAGGTGAGTTATTCAAG 120
QY 1641 GGTGTGTATACACAGATGATTTATGACATGTTGCTTAAGATTGAATCCGTTCTCTATTG 1700
DB 121 GGCTGTGCACACAGATGATTTATGACCTGCTGCTTAAGATTGAATCCACTATTATTATTA 180
QY 1701 CCTGGTGACTTCTCTGCAAAAGGAGAAATGGCAAGGAAATGTATATCATCAAGCAT 1760
DB 181 CCTGGTGACTTCTCTGCAAAAGGAGAAATGGCAAGGAAATGTATATCATCAAGCAT 240
QY 1761 GGAGAGTCCAAAGTCTTCGAGGCCCTGATGATCACTAAAGTCTGGTTACTCTCAAGAGCT 1820
DB 241 GGAGAGTCCAAAGTCTTCGAGGCCCTGATGATCACTAAAGTCTGGTTACTCTCAAGAGCT 300
QY 1821 GGCTCGGTGTTGGAGAAATCAGCTTCTAGCAGCAGGAGGAGAAACCGTCGAACTGCC 1880
DB 301 G-----GCCCTTGGCAAAAGGAGGAAATCGCGGACAGCT 339

```

```

QY 1881 AATGTGGTGGCCACGGGTTTCCCAATCTTTAACTCTAGACAAAGACCCCTCCAGAA 1940
DB 340 GATGTTGTGGCCACGGATTTGCCAATCTTTAACTCTGGCAAAAGACTCTCCAAGAA 399
QY 1941 ATTCTAGTGCATTATCCAGATTCTGAAAGGATCTCTCATGAAGAGCCAGAGTCTTTTA 2000
DB 400 ATTCTGTGCATTATCCCAACTTCTAAAGAGCTCTCATGAAGAGCCCAATTTCTTTTA 459
QY 2001 AAGCAGAGGCTTAAGACCGCAGAGACCCCTCCAGAAAGATCTTGCCTCTCTTTC 2060
DB 460 AGCCAGAGGAGAAACACCACTCAGGCAATCTCTCAAGACCGAGACCTGCTTTTTC 519
QY 2061 CCACCGAAGAGAGACACACCCCAAACTGTTTAAAACTCTCTAGGAGGACAGGAAAGCA 2120
DB 520 CCACCAAGAGAGACACACCCCGAATGCTTTAAAGTTCTCTTAGCACACAGGAAGCTGG 579
QY 2121 AGCTTTGCAGACTACTCAAAATTGAGCGAGAGCAAGCAGCTCAG--AAGAAAGAAATT 2178
DB 580 ACCTTGGAAAGACTCTTTAAGAAAGAGAAACCAACCACTCAGAAATAACGGTGAAA 639
QY 2179 CTGAAGGAGGAGGAGGAGAAAGAAAGAAATGAAGATAAAACAAAGAAATGAAGATA 2238
DB 640 GTTCCACAGGCGAAGAAAGAGAGGAGGAGAGAGATTGAAGACCAAGGAGGACAGACTT 699
QY 2239 AACAAAAGAAATGAAGATAA 2260
DB 700 AGCAGAAAGAAAGAAAGAAAGAA 721
RESULT 7
BX401127 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX401127 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CSODK009YE13 5-PRIME, mRNA sequence.
ACCESSION BX401127
VERSION BX401127
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7817.r For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODK009AC07QPi&cluster=7817.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CSODK009AC07QPi.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK009YE13"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/note="First strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 13.5%; Score 363.8; DB 13; Length 1201;

```

Best Local Similarity 60.8%; Pred. No. 1.9e-49;
Matches 611; Conservative 35; Mismatches 353; Indels 6; Gaps 5;

QY 923 AAATGAGCTAAGGAACACTCAGGACTCTTACAAAATTTTCAGTTGATGTCGATCAAT 982
Dd |||||
8 AAGGATATGGAATACTACTGAGCTTCGCGCTTCAAGATGAGACCTGCTCAGCCT 67
QY 983 AATACATTATGATTTGCTACCTCTTCTTTGGGTTTAATCCAAATGTTAGAGCAATAG 1042
Dd |||||
68 CCGTCCCTTGGATTTCTTATTTGAAAGTCGGTGTGAACCCCTCTCCGCTGCMCG 127
QY 1043 GATGTTAA--GTACACTTCATTTTTCGAATTTAATCATCACCCTAGAGTCTAATGAC 1100
Dd |||||
128 CTGTTTAATGATATCGCCTTCTTCGTTTAAACGCCCTCGGAATCATCTCCTCAGC 187
QY 1101 AAGCATATATCTACAGATTTATTCGAACAACTGGATACTTGCTGTTTATTTCTGCACAT 1160
Dd |||||
188 AAGGCTACGTGTACAGGCTCATCAGGAYCACGYTACCTTCTTACAGCCTGCATTG 247
QY 1161 AATGCTGTGTTTATCTAGGCTTCAAACTATGAAGATTTGCACTACTAGATGGTG 1220
Dd |||||
248 AATTCCTGCTTTATCTAGGCTCGGCTTATCAGGCTCGGCTCCACTCCTCAGCTG 307
QY 1221 TATGATGGGAGGAACAGATCTGAGATGTTTATTTGGGAGTTCGAACCTTAAAT 1280
Dd |||||
308 TACGATGGCTGGGAAACAGTATATTCGCTGTACTTCTGCTGTGAARACWCATC 367
QY 1281 ACCATGCTGGCTTCCAGACCAACAACTTATTTGAATTTGTTTCACTCTGAAT 1340
Dd |||||
368 ATCATCGGGGGCTCGCTCCGACCCCAAGAYACTCTTTGAAATGTCCTCCAGCTGYTGAAT 427
QY 1341 TTTTCTGAGTTTGTGCTTCTCCAGTTTAAATGCTCAGATGAGAGATGTAATGGA 1400
Dd |||||
428 TATTTCAAGGGCTCTTCTGCTGTGATGATGACAGATGAGAGATGTTGATGG 487
QY 1401 CGAGTACAGCCATCAGAACTACTTCGCGCTCGATGATGATGACACCATGCTCATG 1460
Dd |||||
488 GCGGCAACG-CAGACAGCTACTTACCGAGCTGCTGATGACAGACAGCGTGAAGTACATG 546
QY 1461 AACATTAATCTCCATCTTAACTTTGTGCAAAAGCGAGTTCGGAATGTTGATGATATACA 1520
Dd |||||
547 AATTTTCAAGATCCCAAGTCGGTGCAGAAACGAGTCAAGACCTGGTAAGAGTACACC 606
QY 1521 TGGGACTCTCAAGATGATGATGATGCTGATTTGCTTAAGACCTTCAACACTACGCTC 1580
Dd |||||
607 TGGCACTCGAAGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 666
QY 1581 CAGTTAGCCCTCGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1640
Dd |||||
667 CGGCTGGACCTCGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726
QY 1641 GGTGTGATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1700
Dd |||||
727 GGTGTGACCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 786
QY 1701 COTGTGACTTTGTGCAAA--AAAGGGAGAAATTTGCAAGGAAATGATATCATCAAGCA 1759
Dd |||||
787 CCAACGACTATGTGCAAGAAVGGSSAGATCGGCGGTGAGATGATCATCATTCAGGC 846
QY 1760 TGGAGATTCAGTTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATG 1819
Dd |||||
847 AGGCAAGTCAGGCTTGGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 905
QY 1820 TGGTTCGCTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGGAAACCGTCCGAATGCTC 1879
Dd |||||
906 KSSATYTGTTTGSAGAAVAGCTTCTGCTGCTGTTTGGGGCGGCA--DGGGCGCAGCC 964
QY 1880 CAATGTGTGCCCGGCTTGGCAATCTTTAACTCTAGACAA 1924
Dd |||||
965 CAAGTGTGSSSMGGGTTTACMANCTCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTT 1009

RESULT 8

BI827605
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BI827605 832 bp mRNA linear EST 04-OCT-2001
603073571F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5165752 5',
RNA sequence.
BI827605
BI827605.1 GI:15939142
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Mammalia; Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLAM1411 row: m column: 17
High quality sequence stop: 817.

FEATURES
source

Location/Qualifiers
1..832
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5165752"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dr primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen) Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 12.1%; Score 328.4; DB 12; Length 832;
Best Local Similarity 99.4%; Pred. No. 1.2e-43;
Matches 340; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2345 TGCAGTGGAGGAAGAACCCCACTC-AGTTAGAGGACAGTTTACCAGAGGACTTCTC 2403
Dd |||||
1 TGCAGTGGAGGAAGAACCCCACTCAGTTAGAGGACAGTTTACCAGAGGACTTCTC 60
QY 2404 GTCAATCACTCATTTATCAGCATGCTCTTCTGCTGAGGGCGGAGAGAGTTCTTACTA 2463
Dd |||||
61 GTCAATCACTCATTTATCAGCATGCTCTTCTGCTGAGGGCGGAGAGAGTTCTTACTA 120
QY 2464 TTGAAGTCAAGAAAGCTTACCAATAATCTTGAATCTTCTAGATGTATATAGCT 2523
Dd |||||
121 TTGAAGTCAAGAAAGCTTACCAATAATCTTGAATCTTCTAGATGTATATAGCT 180
QY 2524 AGTTCCCAAGTGTATCTAGCTAGGATTTAACTTAAATTAACGAGGGAACGACATGC 2583
Dd |||||
181 AGTTCCCAAGTGTATCTAGCTAGGATTTAACTTAAATTAACGAGGGAACGACATGC 240
QY 2584 TGGACCCCTTGAGAAACGAAAGCAATCCCTAGCTTAGTTCTTAGACTTATCTGAGAG 2643
Dd |||||
241 TGGACCCCTTGAGAAACGAAAGCAATCCCTAGCTTAGTTCTTAGACTTATCTGAGAG 300
QY 2644 TGTGATTTTCATGCTAGTGTATTAAGAGATTTATTAAGGCA 2685
Dd |||||
301 TGTGATTTTCATGCTAGTGTATTAAGAGATTTATTAAGGCA 342

```

RESULT 9
AA069559
LOCUS
DEFINITION
  zf78a04.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
IMAGE:382734 5', mRNA sequence.
ACCESSION
AA069559
VERSION
AA069559.1 GI:1576971
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 468)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaskis,B., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 874 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 382.
Location/Qualifiers
1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1290991"
/db_xref="taxon:9606"
/clone="IMAGE:382734"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_pineal_gland_N3HPG"
/notes="Organ: pineal gland; Vector: p773D (Pharmacia)
with a modified polylinker; Site.1: Not I; Site.2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified p773
vector (Pharmacia). Library constructed by Bento Soares
and M.Patima Bonaldo."

FEATURES
source
1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1290991"
/db_xref="taxon:9606"
/clone="IMAGE:382734"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_pineal_gland_N3HPG"
/notes="Organ: pineal gland; Vector: p773D (Pharmacia)
with a modified polylinker; Site.1: Not I; Site.2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified p773
vector (Pharmacia). Library constructed by Bento Soares
and M.Patima Bonaldo."

ORIGIN
Query Match 11.9%; Score 320.8; DB 9; Length 468;
Best Local Similarity 97.9%; Pred. No. 2.8e-42;
Matches 325; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 81 AAGTCAACAGGTGAAGCTATAGGAGAGAACAAATGAGTAAGCAAAAGTTCTCGTGG 140
Db 2 AAAGTCAACAGGTGAAGCTATAGGAGAGAACAAATGAGTAAGCAAAAGTTCTCGTGG 61
Cy 141 AATGAAGAGGCTCTCAACCAAGTAATCACTTCAGCAACACACAGGAGGAAAC 200
Db 62 AATGAAGAGGCTCTCAACCAAGTAATCACTTCAGCAACACACAGGAGGAAAC 121
Cy 201 AAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACGTCTGAAGAGCCACAC 260
Db 122 AAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCACGTCTGAAGAGCCACAC 181

```

```

261 ACCAACATACAGACAAACTCTCCAGAAATTTCTCTGGAGATCTGACCAACACCT 320
182 ACCAACATACAGACAAACTCTCCAGAAATTTCTCTGGAGATCTGACCAACACCT 241
321 GACCTCAAATGCAGACAGAACCAACTGGAACAGTCCAGAGCAGAGGAATGGACCCC 380
242 GACCTCAAATGCAGACAGAACCAACTGGAACAGTCCAGAGCAGAGGAATGGACCCC 301
381 GGGAAAGAGGTTCACACAGCCCAACAAACAA 412
302 GGGAAAGAGGTTCACACAGCCCTAGAA 333

H53423 445 bp mRNA linear EST 20-SEP-1995
Yc86a09.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
IMAGE:231160 5', mRNA sequence.
H53423
ACCESSION
H53423
VERSION
H53423.1 GI:993570
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 445)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaskis,B., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 903
High quality sequence stop: 302
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 903 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 302.
Location/Qualifiers
1..445
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3861151"
/db_xref="taxon:9606"
/clone="IMAGE:231160"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_pineal_gland_N3HPG"
/notes="Organ: pineal gland; Vector: p773D (Pharmacia)
with a modified polylinker; Site.1: Not I; Site.2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified p773
vector (Pharmacia). Library constructed by Bento Soares
and M.Patima Bonaldo."

ORIGIN
Query Match 11.7%; Score 317; DB 14; Length 445;
Best Local Similarity 91.1%; Pred. No. 1.2e-41;

```

Matches 349; Conservative 0; Mismatches 27; Indels 7; Gaps 1;

QY 25 CATAAATACAGAGGTTTTCAGAACACCTCAGAGAGATGTTTAAATCGCTGACAAAAG 84
 Db 1 CATAAATACAGAGGTTTTCAGAACACCTCAGAGAGATGTTTAAATCGCTGACAAAAG 60

QY 85 TCAACAAGGTGAAGCCTATAGGAGAGAAACAATGAGAAATGAAACAAGTTCTCGTGGAAATG 144
 Db 61 TCAACAAGGTGAAGCCTATAGGAGAGAAACAATGAGAAATGAAACAAGTTCTCGTGGAAATG 120

QY 145 AAGAAGGCTCTACCCCAAGTAATCACTCTCAGCAACACACAGCAGAGGAGAAACAAAG 204
 Db 121 AAGAAGGCTCTACCCCAAGTAATCACTCTCAGCAACACACAGCAGAGGAGAAACAAAG 180

QY 205 GTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCAAGTCTGAGAGGACACACCA 264
 Db 181 GTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTCAAGTCTGAGAGGACACACCA 240

QY 265 ACATACAGACAAACTCTCAAGAAAATTCCTCTGGAGATCTGACCAACAAACCTTGACC 324
 Db 241 ACATACAGACAAACTCTCAAGAAAATTCCTCTGGAGATCTGACCAACAAACCTTGACC 300

QY 325 CTCAAAATGACAGACAGAACCACTGGAACAGTGCAGAGCAGAGGAAATGGA-----C 377
 Db 301 CTCAAAATGACAGAGGACCACTGGAACAGTGCAGAGCAGAGGAAATGGAATGGGACCC 360

QY 378 CCCGGGAAAGAGTCCAAACAG 400
 Db 361 CCGGGAAGGAGTNCACACAG 383

RESULT 11
 BQ068992 978 bp mRNA linear EST 02-APR-2002
 LOCUS AGENCOURT 6740166 NIH_MGC_47 Homo sapiens cdna clone IMAGE:5802872
 DEFINITION 5', mRNA Sequence.

ACCESSION BQ068992
 VERSION BQ068992.1 GI:19898038
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 978)

NIH-MGC <http://mgs.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LUCM2037 row: p column: 09

High quality sequence stop: 726.

Location/Qualifiers

1..978

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5802872"

/tissue_type="neuroblastoma, cell line"

/lab_host="NIH MGC_47"

/clone_lib="NIH MGC_47"

/note="Organ: brain; Vector: pOTB7; Site: 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

FEATURES
 source

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 11.4%; Score 308.4; DB 13; Length 978;
 Best Local Similarity 67.7%; Pred. No. 2e-40;
 Matches 432; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

QY 1388 AGATGTGATTGGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCCTGCGATGGATGACAC 1447
 Db 1 AGATGTGTTAGGGCGCGCCACCGGGGACAGACCTACTACCGCAGCTGCGATGGAGCAGCAC 60

QY 1448 CATTCGCTACATGACAACTTACTCCATTCCTAACTTGTGCAAAAGCGAGTTCGGACTTG 1507
 Db 61 GGTGAAGTACATGATGAAATTTCTACAAGATCCCAAGTCCCGTGCAGAACCGCGTCAAGACCTG 120

QY 1508 GTATGAATATACATGGGACTCTCAAGAAATCTAGATGAGTCTGATTTGCTTAAGACCT 1567
 Db 121 GTACGAGTACACCTGGCACTCGAAGGCATGCTGGATGAGTCAAGCTGATGGTGCAGCT 180

QY 1568 ACCAACTACGGTCCAGTTAGCCCTGCGCAATGATGTGAACCTCAGCATCATCAGCAAGT 1627
 Db 181 TCCAGACAAGATGCGGCTGGACCTCGCCATCGAGTGAACCTACACATCGTTAGCAAGT 240

QY 1628 CGACTTGTTCAGGGTGTGTGATACACAGATGATTTATGACATGTTTCTTAAGATTGAAATC 1687
 Db 241 CGACTTGTTCAGGGTGTGTGATACACAGATGATTTATGACATGTTTCTTAAGATTGAAATC 300

QY 1688 CGTCTCTATTTGCTGCTGAGTCTTGTCTGCAAAAGGAGAAATGGCAAGAAATGTA 1747
 Db 301 TGTGTCTACTTCCCAACGACTATGTGTGCAAGAGGGGAGATCGGCGCTGAGATGTA 360

QY 1748 TATCATCAAGCATGAGAGAGTCCAAAGTCTTGGAGGCCCTGATGTTACTAAAGTTCTCGT 1807
 Db 361 CATCATCCAGGAGGAGGAGTGCAGTCTTGGCGGCCCTGATGGGAATCTGTGCTCGT 420

QY 1808 TACTCTGAAAGCTGGTGGTCTTTTGGAGAAATCAGCCTTCTTAGCAGCAGGAGGAGAAA 1867
 Db 421 GACGCTGAAAGCTGGTCTGTGTTTGGAGAAATAAGTCTGCTGGCTGTGTGGGGCGGAAA 480

QY 1868 CCGTGAAGTCCCAATGGTGGCGCCACGGTTCCTCCAACTCTTTTAACCTAGACAAA 1927
 Db 481 CCGGCGCAGCGCCAAACGTTGGTGGCGCACGGGTTTACCAACCTCTTCATCCTCGAAGAA 540

QY 1928 GACCTCCCAAGAAATCTAGTGCATTATCCAGATCTGAAAGATCCTCATGAAGAAAGC 1987
 Db 541 GGAACCTGAATGAGATTTGTTGCAATTCTGAGTCTCAGAGTTACTCCGGAAGAAAGC 600

QY 1988 CAGAGTGCTTTTAAAGCAGAGGCTTAAGACCCGCAAG 2025
 Db 601 CAGGCGCATGCTGAGAAGCAACAATAAGCCCAAGAGG 638

RESULT 12

AU137778

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AU137778 694 bp mRNA linear EST 02-AUG-2002
 AU137778 PLACE1 Homo sapiens cdna clone PLACE1007225 5', mRNA
 sequence.

AU137778

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 694)
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Cta,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

HRI human cDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

source
 1. .694
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="PLACE1007225"
 /tissue_type="placenta"
 /clone_lib="PLACE1"
 /note="Vector: pME189FL3"

ORIGIN

Query Match 11.2%; Score 301.4; DB 9; Length 694;
 Best Local Similarity 66.3%; Pred. No. 3.2e-39;
 Matches 445; Conservative 0; Mismatches 225; Indels 1; Gaps 1;
 QY 1111 TCTACAGAGTTATTCGAACAACCTGGATCTCTGCTTTTATTCGACATTAATGCTG 1170
 Db 20 TCTGAGGGTATCAGGACCAAGCTTCTCTACAGCTGCAATTTGAATTCCTGTC 79
 QY 1171 TTTATATCGGCTTCAAACTATGAAGAAATGGCACTATAGATGGTGTATGATGGG 1230
 Db 80 TTTATATCGGCTTCAAACTATGAAGAAATGGCACTATAGATGGTGTATGATGGG 139
 QY 1231 AAGGAACAGATCTGAGATGTTATTTATGGCAGTCGAACTTATACCAATGGTG 1290
 Db 140 TCGGAACAGTATATTCGCTGTTACTACTTGTCTGTGAAGACCTCATCACCACGGG 199
 QY 1291 GCCTTCCAGAACCAAACTTTATTTGAATTTGTTTCACTCTGAAATTTTTTTCTG 1350
 Db 200 GGCTGCTGACCCCAAGACACTTTTGAATTTGTTTCCAGCTCTGAAATTTTCAAG 259
 QY 1351 GAGTTTGTGTTCTCCAGTTAATTTGTGATGAGATGATGATGGAGCAGCTACAG 1410
 Db 260 GCGTCTTGTCTCTGTGATGATCGACAGATGAGATGTTGTAGGGCGCGCCACCG 319
 QY 1411 CCAATCAGAACTACTTCCGCGCTGCAATGATGACACCACTGCTCATGAACAATTA 1470
 Db 320 CGGACAGACCTACTACCGAGCTGCATGGACAGCAGGTGAAGTACATGAATTTCTA 379
 QY 1471 CCATTCCTAACTTGTGCAAAAGCAGTTGGACTTGGTATGATATACATGGAGCTTC 1530
 Db 380 AGATCCCCAAGTCCGTGCGAGAACCGCTCAAGACCTGGTACGATACACCTGGCACTCG 439
 QY 1531 AAAGAATCTAGATGAGTCTGATTTGTTTGAACCTTACCACTACCGTCCAGTTAGCCC 1590
 Db 440 AAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 499
 QY 1591 TCGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1650
 Db 500 TCGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 559
 QY 1651 CACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1710
 Db 560 GGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 619
 QY 1711 TTGTTCTGAAA-AAGGGAGAAATTTGGCAAGGAATTTATATCATCAAGCATGAGAGTC 1769
 Db 620 ATGTGTGCAAGAGGGGAAATCGGCGTGTGATGATGATGATGATGATGATGATGATG 679
 QY 1770 CAAGTTCTTG 1780
 Db 680 CAAGGTCNTGG 690

RESULT 13

BX104558 741 bp mRNA linear EST 06-FEB-2003
 BX104558 Soares pineal gland 3NBHPC Homo sapiens cDNA clone
 IMAGE:384252, mRNA sequence.
 IMAG998P13890 ; IMAGE:384252, mRNA sequence.
 BX104558
 BX104558.1 GI:27832995
 EST.
 Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 741)
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radloff, U., Schneider, D. and Korn, B.
 Human Unigeneset - RZPD3
 Unpublished (2003)
 Contact: Ina Rolfes
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAG998P13890.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No. 972)
 http://www.rzpd.de/CloneCards/cgi-
 bin/showLib.pl.cgi/responder?libNo=972 Contact: Ina Rolfes
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source
 1. .741
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAG998P13890 ; IMAGE:384252"
 /tissue_type="brain, pineal gland"
 /dev_stage="adults (ages 18, 20, 48)"
 /lab_host="DH10B"
 /clone_lib="Soares pineal gland 3NBHPC"
 /note="1st strand cDNA (prepared from post mortem tissue)
 was primed with a Not I - oligo(dT) primer [5',
 TGTTACCAATCTGAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to EcoRI adaptors
 5'-AATTCGACCGAGG-3' and 5'-CCTCGTGGCG-3' (Pharmacia),
 digested with NotI and cloned into the NotI and EcoRI
 sites of the pT73D-Paci vector. Library went through one
 round of normalization, to Cot38. Library constructed by
 Bento Soares and M. Fatima Bonaldo"

ORIGIN

Query Match 10.6%; Score 286.8; DB 13; Length 741;
 Best Local Similarity 97.7%; Pred. No. 7.2e-37;
 Matches 291; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 115 ATGAGAATGACAAAGTTCTCGTGGATGAGAGGCTCTCACCCAGTATCAGTCTC 174
 Db 1 ATGAGAATGACAAAGTTCTCGTGGATGAGAGGCTCTCACCCAGTATCAGTCTC 60
 QY 175 AGCAACACACAGCAGGAGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAA 234
 Db 61 AGCAACACACAGCAGGAGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAA 120
 QY 235 CTCAGTCACTCTGAGAGCCACACACCACTACAGACAACTCTCCAGAGAAATTT 294
 Db 121 CTCAGTCACTCTGAGAGCCACACACCACTACAGACAACTCTCCAGAGAAATTT 180
 QY 295 CCTCTGGAGATCTGACCAAAACCTCTGACCTCAAAATGCGAGAGAACCACTGGAAACAG 354

```

Db      181 CCTCTGGAGATCTGACCACAAACCCCTGACCCCTCAAATGCAGCAGAACCAACTGGAACAG 240
Qy      355 TGCAGAGGAGAGGAAATGGACCCCGGGAAGAAGTCCAAACACGCCCCACAAACAA 412
Db      241 TGCAGAGCAGAGGAAATGGACCCCGGGAAGAAGTCCAAACACAGTTGACCCCTAGAA 298

RESULT 14
B1736222
LOCUS      603359912F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5367194 5',
DEFINITION mRNA sequence.
ACCESSION B1736222
VERSION    B1736222.1 GI:15713235
KEYWORDS   EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    1 (bases 1 to 738)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgaps-remail.nih.gov
              Tissue Procurement: The Cepko Laboratory
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM11934 row: g column: 03
              High quality sequence stop: 736.

FEATURES             source
    source
        1..738
            Location/Qualifiers
                1..738
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:5367194"
                    /tissue_type="retina"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_94"
                    note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
                    Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
                    Average insert size 3.3 kb. Library enriched for
                    full-length clones and constructed by Life Technologies.
                    Note: this is a NIH_MGC Library."

ORIGIN
Query Match      10.4%; Score 280.8; DB 12; Length 738;
Best Local Similarity 63.0%; Pred. No. 6.7e-36;
Matches 466; Conservative 0; Mismatches 272; Indels 2; Gaps 2;

Qy      810 ATACACTACTGGCTTATTCGGACATCATATGTGATATCATCTACCTTTATGATATGCTA 869
Db      1 ATCCACTTCGGCTCTCATGATTAATCTTGGCACTTCATCTACCTCTCGACATCACC 60
Qy      870 TTATTCAGCCAGACTCCAGTTTGTAAAGAGAGAGACATAATAGTGGATCAATGAG 929
Db      61 GTGTTCCAGATGCGGCTGCGAG-TTGTCAAAGCGGGGACATCATTTACAGACAAGAGGAG 119
Qy      930 CTAAGGAACACTACAGACTTCTACAAAATTTTCAGTTGGATGTGCGATCAATAATACCA 989
Db      120 ATGCGATAATAACTACTTGAACCTTGGCATCAACCTCTCTTGGCTGCCCGCTGCTG 179
Qy      990 TTGTGATATTGTACTCTCTTTGGGTTTATCCAAATGTTTAGAGCAAAATAGGATGTTA 1049
Db      180 TTGACTTTCTACTTGAACCTTGGCATCAACCTCTCTTGGCTGCCCGCTGCTG 239
Qy      1050 AAGTACACTTCAATTTTGAATTTATCATCACTAGAGTCTATAATGGACAAAGCATAT 1109
Db      240 AAGTACATGGCCCTTCTTTGAGTTTAAACCGCCTGGGAAGCCATCTCAGCAAAAGCCTAC 299

```

```

Qy      1110 ATCTACAGAGTATTTCGAACAACCTGGATACTTGTGTTTATTTCTGCAATTAATGCGCTGT 1169
Db      300 GTTTCACAGAGTCATCAGGACCAACGGCTTACCTGCTGTACAGCTGCACTCAACTCCTGC 359
Qy      1170 GTTATTACTGGCTTCAAACTATGAAGGAATTCGCACTACTAGATGGTGTATGATGGG 1229
Db      360 CTTTACTACTGGCATCAGCCT-TCCAGGCACTCGCTCCACTCACTGGGTTTACACGGA 418
Qy      1230 GAAGGAAACGAGTATCTCAGATGTTATTATTGGGCACTTCCAACTTTAATTAATTAATGCT 1289
Db      419 GTGGGGAACAGTTATTTCGATGCTACTTACCTGGCTGTGAAACCCCTCATCACCATCGGA 478
Qy      1290 GGCCTTCGAGAACCAACAACTTTATTGAAATGTTTTCACACTTGAATTTTCTTCT 1349
Db      479 GGACTGCCCGACCCCGACAGCGCTCTTTGAGATTGCTTCCAGCTGCTGAATTTTACC 538
Qy      1350 GGAGTTTTTGTCTCTCCAGTTTAAATGTCAGATGAGAGATGTGATTGGAGCAGCTACA 1409
Db      539 GGGGTTCTTGTCTCTCTGATGATTCGACAGATGAGAGATGTGTGGGGCCGCCACA 598
Qy      1410 GCCAATCAGAACTACTTCCGGCCCTGCATGGATGACACACCATTCCTACATGACAAATAC 1469
Db      599 GCGGGGACAGCTACTACCGCAGCTGCATGGACACACAGTGAAGTACATGAATCTTAC 658
Qy      1470 TCCATTCTCTAACTTGTGCARAAGCGAGTTCGGACTTGTGATGAATATACATGGGACTCT 1529
Db      659 AAGATCCCGAGTGTGTGCAGAACCGTGTCAAGACCTGGTATGAGTACACCTGGCATTCG 718
Qy      1530 CAAAGAATGCTAGATGAGTC 1549
Db      719 CAAGGCATGCTGATGAGTC 738

RESULT 15
AV726367      758 bp mRNA linear EST 16-OCT-2000
LOCUS      AV726367 HTC Homo sapiens cDNA clone HTCCDC01 5', mRNA sequence.
DEFINITION AV726367
ACCESSION AV726367
VERSION    AV726367.1 GI:10832695
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    1 (bases 1 to 758)
AUTHORS      Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
              Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
              Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
              Chen, J., Chen, Z. and Han, Z.
              Homo sapiens cDNA HTC clones
              Unpublished (2000)
              Contact: Zeguang Han
              Chinese National Human Genome Center at Shanghai
              351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
              201203, P. R. China
              Tel: 86-21-50801919 (ex.45)
              Fax: 86-21-50801922
              Email: hanzg@chgc.sh.cn
              This clone is available at CHGC in Shanghai.

FEATURES             source
    source
        1..758
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="HTCCDC01"
            /tissue_type="Hypothalamus"
            /dev_stage="Adult"
            /lab_host="SOLR"
            /clone_lib="HTC"
            /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
            XhoI"

ORIGIN

```



```

Query Match      10.4%; Score 280.4; DB 9; Length 758;
Best Local Similarity 99.8%; Pred. NO. 7.7e-36;
Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2404 GTCAATCACTCATTTATCAGCATGGCTTCCTTCGCTGAGGGCGGAGAGAGGTTCTTACTA 2463
Db 1 GTCAATCACTCATTTATCAGCATGGCTTCCTTCGCTGAGGGCGGAGAGAGGTTCTTACTA 60

QY 2464 TTGAAGTCAAAGAAAGGCTAAGCAATAAATGTTTGATTTATCTTTAGATGTGATATAGCT 2523
Db 61 TTGAAGTCAAAGAAAGGCTAAGCAATAAATGTTTGATTTATCTTTAGATGTGATATAGCT 120

QY 2524 AGTTCCCAAAGTGATTGTACCTAGGATTGTTAACTTAAATTAACGAGGGGGAACGACATGC 2583
Db 121 AGTTCCCAAAGTGATTGTACCTAGGATTGTTAACTTAAATTAACGAGGGGGAACGACATGC 180

QY 2584 TGGGACCCCTTGAGAAACGAAAGGCAAAATCCCTAGCTTAGTTTCTAGGACTTATCTGAGAG 2643
Db 181 TGGGACCCCTTGAGAAACGAAAGGCAAAATCCCTAGCTTAGTTTCTAGGACTTATCTGAGAG 240

QY 2644 TGTGATTTTCATGCAGTGGTAATARGAGATTATTAAAGCAA 2685
Db 241 TGTGATTTTCATGCAGTGGTAATARGAGATTATTAAAGCCA 282

```

Search completed: June 22, 2004, 04:03:28
Job time : 6766.81 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 18:22:44 ; Search time 183.254 Seconds
(without alignments)
8185.526 Million cell updates/sec

Title: US-09-855-828-2
Perfect score: 2703
Sequence: 1 cattctctaccttaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
C 1	100.8	3.7	7218	1	US-08-232-463-14
2	85.6	3.2	2223	1	US-08-257-073-4
C 3	78.8	2.9	929	4	US-09-671-317-14
C 4	72.8	2.7	1001	4	US-09-671-317-439
C 5	66.6	2.5	396	4	US-09-640-173-53
C 6	66.6	2.5	396	4	US-09-713-550-53
7	66.2	2.4	2394	4	US-08-800-729-33
8	65.6	2.4	1696	4	US-09-835-811-1
9	65.6	2.4	2447	2	US-09-014-969-14
10	64.8	2.4	43795	3	US-08-742-185-101
11	64.2	2.4	240	1	US-08-628-417-6
12	64	2.4	1447	4	US-09-443-041A-27
13	63	2.3	674	4	US-09-620-405B-465
14	63	2.3	674	4	US-09-433-826B-465
15	63	2.3	674	4	US-09-604-287A-465
16	63	2.3	674	4	US-09-834-759-465
17	62.8	2.3	1051	3	US-09-245-041-10
C 18	62.6	2.3	118067	4	US-09-497-855A-32
C 19	62.2	2.3	16442	3	US-08-781-891-208
C 20	62.2	2.3	16442	4	US-09-618-166-208
21	61.6	2.3	249	4	US-09-621-976-1322
22	61.6	2.3	2608	4	US-09-904-615-16
23	61.6	2.3	3211	3	US-08-574-959A-8
24	61.6	2.3	3211	2	US-09-357-014-8
25	61.6	2.3	3901	2	US-08-574-959A-6
26	61.6	2.3	3901	3	US-09-357-014-6
27	61.4	2.3	282	3	US-09-461-697-205

28	61.4	2.3	306	3	US-09-461-697-203	Sequence 203, App
29	61.4	2.3	696	3	US-09-461-697-193	Sequence 193, App
30	61.4	2.3	699	3	US-09-461-697-191	Sequence 191, App
31	61.4	2.3	717	3	US-09-461-697-189	Sequence 189, App
32	61.4	2.3	774	3	US-09-461-697-187	Sequence 187, App
33	61.4	2.3	819	3	US-09-461-697-185	Sequence 185, App
34	61.4	2.3	1669	3	US-09-461-697-184	Sequence 184, App
35	60.8	2.2	1798	4	US-09-797-306-1	Sequence 1, Appli
C 36	60.8	2.2	12980	4	US-08-811-566-5	Sequence 5, Appli
C 37	60.8	2.2	12980	4	US-09-034-756-5	Sequence 5, Appli
38	60.4	2.2	5394	4	US-08-688-376-1	Sequence 1, Appli
39	59.6	2.2	240	4	US-09-621-976-1324	Sequence 1324, Ap
40	59.6	2.2	5152	4	US-10-204-708-47	Sequence 47, Appl
41	59.2	2.2	55298	4	US-09-491-356C-1	Sequence 1, Appli
42	59	2.2	231	3	US-09-461-697-207	Sequence 207, App
43	58.6	2.2	569	4	US-09-461-325-44	Sequence 44, Appl
44	58.6	2.2	569	4	US-10-012-542-44	Sequence 44, Appl
45	58.4	2.2	1276	3	US-09-177-325-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ5pT-Fls
; US-08-232-463-14

Query Match 3.7%; Score 100.8; DB 1; Length 7218;

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-014-969-14

Query Match 2.4%; Score 65.6; DB 2; Length 2447;
Best Local Similarity 56.0%; Pred. No. 9.2e-07;
Matches 122; Conservative 1; Mismatches 95; Indels 0; Gaps 0;

QY 2091 AAACTCTCTAGAGGCACAGGAAAGCAAGTCTTGCAGAGACTACTCAAAATTGAAGCGA 2150
DB 2229 ATAAACCTTTTGGAGGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 2288
QY 2151 GAGCAACGACCTCAGAGAAAGAAATCTGAAGGAGGAGGAGGAGGAGGAGGAGG 2210
DB 2289 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2348
QY 2211 GAAGATTAACCAAAAGAAATGAGATTAACCAAAAGCAAAATGAAGTAAAGCAAGAA 2270
DB 2349 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2408
QY 2271 AATGAAGATAAGATAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2308
DB 2409 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2446

RESULT 10
US-08-742-185-101
Sequence 101, Application US/08742185
Patent No. 6020476
GENERAL INFORMATION:
APPLICANT: Page, David C.
APPLICANT: Reijo, Renee
APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-JUL-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH194-07A2
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 43795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match 2.4%; Score 64.8; DB 3; Length 43795;
Best Local Similarity 63.5%; Pred. No. 6.1e-06;
Matches 99; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 2149 GAGCAACGACCTCAGAGAAAGAAATCTGAAGGAGGAGGAGGAGGAGGAGGAGG 2208
DB 38894 GAGATGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 38953
QY 2209 ATGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAAGAAAGAAAGAAAGAA 2268
DB 38954 AGGAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 39013
QY 2269 AAAATGAAGATAAAGATAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2304
DB 39014 AAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 39049

RESULT 11
US-08-628-417-6
Sequence 6, Application US/08628417
Patent No. 5627054
GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
ADDRESSEE: DEFENSE COMMAND
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
STATE: MARYLAND
COUNTRY: USA
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 398-94
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 bases
TYPE: nucleic acid

Db 552 AAA 611
Qy 2230 ATCAAGATTAACAAAAGAAATGAGATAAAGGAAAGAAAATGAAGATAAAGATAAG 2289
Db 612 AAA 671
Qy 2290 GAA 2292
Db 672 AAA 674

RESULT 15
US-09-604-287A-465
; Sequence 465, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 465
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-465

Query Match 2.3%; Score 63; DB 4; Length 674;
Best Local Similarity 59.0%; Pred. No. 2.2e-06;
Matches 108; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
Qy 2110 CAGGAAAGCAAGTCTTTCAGAGACTACTCAAATTGAGCGAGAGCGAGCTCAGAAGA 2169
Db 492 CAGCAAAAGGAGACCTAGGAAGATCGCATGGGAGAAAAGATGACTCAGTTAAGGCAA 551
Qy 2170 AAGAAATTCGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2229
Db 552 AAA 611
Qy 2230 ATGAAGATAAACAAAAAGAAAATGAGATTAAGGAAAGAAAATGAAGATAAAGATAAG 2289
Db 612 AAA 671
Qy 2290 GAA 2292
Db 672 AAA 674

Search completed: June 22, 2004, 04:09:24
Job time : 190.254 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 00:29:50 ; Search time 1106.37 Seconds
(without alignments)

11192.162 Million cell updates/sec

Title: US-09-855-828-2

Perfect score: 2703

Sequence: 1 cattctctacttaaggca.....aaaaaaaaaaaaaaaaaaaaa 2703

Scoring table:

IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	577.4	21.4	2607	16	US-10-189-507-3
2	577.4	21.4	4382	16	US-10-159-563-147
3	306	11.3	680	13	US-10-027-632-204539
4	306	11.3	680	16	US-10-027-632-204539
5	176.4	6.5	2500	13	US-10-342-887-427
6	176.4	6.5	2500	13	US-10-172-118-427
7	133.2	4.9	3027	15	US-10-295-573-1
8	132.8	4.9	2085	15	US-10-345-680-27
9	132.8	4.9	1995	15	US-10-345-680-25
10	131.6	4.9	1995	15	US-10-087-217-1
11	131.6	4.9	1995	15	US-10-087-217-5
12	131.6	4.9	3027	15	US-10-295-573-2
13	131.6	4.9	3027	15	US-10-295-573-4
14	129	4.8	526	9	US-09-864-761-12975

15	128.4	4.8	1995	15	US-10-087-217-3	Sequence 3, Appli
16	128.4	4.8	1995	15	US-10-087-217-7	Sequence 7, Appli
17	128	4.7	2877	15	US-10-295-573-3	Sequence 3, Appli
18	127	4.7	127	9	US-09-864-761-29538	Sequence 29538, A
19	111.2	4.1	1995	9	US-09-795-927-1	Sequence 1, Appli
20	111.2	4.1	1995	14	US-10-034-843-1	Sequence 1, Appli
21	111.2	4.1	1995	15	US-10-168-651-34	Sequence 34, Appli
22	111.2	4.1	1995	16	US-10-189-507-1	Sequence 1, Appli
23	111.2	4.1	2111	15	US-10-114-153-17	Sequence 17, Appli
24	111.2	4.1	2190	15	US-10-029-677-23	Sequence 23, Appli
25	111.2	4.1	12017	9	US-09-795-927-3	Sequence 3, Appli
26	109.6	4.1	1995	16	US-10-189-507-4	Sequence 4, Appli
27	109.6	4.1	2186	15	US-10-029-677-1	Sequence 1, Appli
28	84	3.1	31124	13	US-10-087-192-463	Sequence 463, App
29	81	3.0	625	13	US-10-027-632-179350	Sequence 179350,
30	81	3.0	625	16	US-10-027-632-179350	Sequence 179350,
31	80	3.0	2332	15	US-10-087-464-45	Sequence 45, Appli
32	79.6	2.9	305	9	US-09-864-761-19262	Sequence 19262, A
33	79.6	2.9	496	9	US-09-864-761-2534	Sequence 2534, Ap
34	79.2	2.9	37265	13	US-10-087-192-49	Sequence 49, Appli
35	79.2	2.9	39443	16	US-10-085-117-313	Sequence 313, App
36	79	2.9	276	9	US-09-864-761-20595	Sequence 20595, A
37	79	2.9	462	9	US-09-864-761-3829	Sequence 3829, Ap
38	79	2.9	1728	9	US-09-927-267-3	Sequence 3, Appli
39	79	2.9	1728	16	US-10-189-507-2	Sequence 2, Appli
40	79	2.9	2308	9	US-09-927-267-2	Sequence 351, App
41	79	2.9	2366	13	US-10-302-172-351	Sequence 29, Appli
42	79	2.9	2551	10	US-09-842-758-29	Sequence 14, Appli
43	79	2.9	2551	13	US-10-174-333-29	Sequence 15, Appli
44	78.8	2.9	929	13	US-10-294-934-14	
45	78.6	2.9	143899	10	US-09-972-546-15	

ALIGNMENTS

RESULT 1

US-10-189-507-3
; Sequence 3, Application US/10189507
; Publication No. US20030228633A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: MOYER, BRYAN
; APPLICANT: PRONIN, ALEX
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: SERVANT, GUY
; APPLICANT: CALLAMARAS, NICHOLAS
; TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
; TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
; TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
; TITLE OF INVENTION: SMELL MODULATORS
; FILE REFERENCE: 078003-0291567
; CURRENT APPLICATION NUMBER: US/10/189,507
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/303,140
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/337,154
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-189-507-3
Query Match 21.4%; Score 577.4; DB 16; Length 2607;
Best Local Similarity 64.3%; Pred. No. 9.6e-119;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;
QY 679 TTCGAAACAGCATGATTCTACAGATCGACTCTATCTCCCTGCTCTTGTCTCA 738

Db 782 TTCCCCAGAGCATGTGACCCGCTGACCAACCTGATGTATGCTATGGCTGTCTTCGTGG 841
QY 739 CTCTTGCCCTATACTGGAAGTCTGTTTATACCACTGGCGCTGCTCTTCCCATATCAA 798
Db 842 TGATGSCCTGGAAATGGAACTGTGGCTGTTCCCGTGGCTGGGCTTCCCTTACCAGA 901
QY 799 CCGCAGACAACATACACTACTGCTGTTATGCGGACATCATATGTGATATCATCTACCTTT 858
Db 902 CCCCGACAAACATCCACCACTGGCTGCTGATGGATTAACCTATGCGACCTCATCTACTTCC 961
QY 859 ATGATATGCTATTTATTCAGCCAGACCTCCAGTGTGTAAGAGGAGACATATAGTGG 918
Db 962 TGGACATACCGGTGTTCCAGACACCGCTGCACTTTGTGAGAGGGGGGACATCATACGG 1021
QY 919 ATTCAATGAGCTAAGGAAACACTACAGACTTCTACAAAATTTTCAGTTGGATGTGCGAT 978
Db 1022 ACAAAGGACATGCGAATAACTACCTGAAGTCTCGCGCTTCAAGATGACCTGTCTCA 1081
QY 979 CAATAATACCATTTGATATTTGCTTACCTCTCTTTGGGTTTAAATCCAAATGTTTAAAGCAA 1038
Db 1082 GCTCTGCGCTGTGATTTCTCTATTTGAAAGTGGGTGTAACCCCTCTCCGCGCTGC 1141
QY 1039 ATAGGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCACTAGAGTCTATATAGG 1098
Db 1142 CCGCTGTTTAAAGTACATGCGCTTCTTCGAGTTTAAACAGCGGCTGGAATCCATCTCA 1201
QY 1099 ACAAGCATATATCTACAGAGTTATCGAAACAATGGAATCTCTGTTTATCTGACACA 1158
Db 1202 GCAAGCCTACGTGTACAGGCTTATCAGACACACAGCCTACTCTCTACAGCCTGCATT 1261
QY 1159 TTAAGCCTGTGTTTATTAATGCGCTTCAAACTATGAAGGAATGCGCACTAGATGGG 1218
Db 1262 TGAATCTGTTTATTTACTGCGCATCGGCTTATCAGGGCTCGGCTCCACTCAGTGG 1321
QY 1219 TGTATGATGGGAGGAAACAGATCTGAGATGTTTATTTGGGAGTTTGAACCTTTAA 1278
Db 1322 TTTAGATGGGCTGGGAAACAGTTATTTCTGCTGTACTTCTGCTGTGAAGCCCTCA 1381
QY 1279 TTACATGTGGCTTCCAGAACCAACAATTTATTTGAATTTGTTTCAACTCTGA 1338
Db 1382 TCACATCGGGGGCTGCTGACCCCAAGACACTCTTTGAATTTGCTTCCAGCTGCTGA 1441
QY 1339 ATTTTCTGAGTGTGTTTGTGTTTCTCCAGTTTAAATTTGTCAGATGAGAGATGTGATTG 1398
Db 1442 ATTTTTCACGGCGTCTTGTCTGCTGATGATCGGACAGATGAGAGATGTGTTAG 1501
QY 1399 GAGCAGCTACAGCAATCAGAACTACTTCCGCGCTGCTGATGATGACACCAATTTGCCCTACA 1458
Db 1502 GGGCGGCAACCGGGGACAGACTTACTACCGGAGCTGATGGACAGCACGCTGAAATGTA 1561
QY 1459 TGAACAATTTACTCCATTTCTTAAACTTGTGAAAGCGAGTTTCGACTTGTGATGATATA 1518
Db 1562 TGAATTTCTACAGATCCCAAGTCCGCTGAGAACCCGCTCAAGACTGTGATGATATA 1621
QY 1519 CATGGGACTCTCAAGAAATGCTAGATGATGCTGATTTGCTTAAAGCCCTACCAACTACGG 1578
Db 1622 CTTGGCACTCGCAAGGATGCTGGATGAGTCAGAGCTGATGTTGCTGCAAGCAAGA 1681
QY 1579 TCCAGTTAGCCCTCGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1638
Db 1682 TGGGCTGAGACTCGCCATCGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1741
QY 1639 AGGGTGTGATACAGATGATTTGACATGTTGCTAAGATTTGAATCCGTTCTCTATT 1698
Db 1742 AGGGCTGTGACCGGACATGATCTTTGACATGCTGAAGAGGCTTCGCTCTGTTGCTACC 1801
QY 1699 TGCTGTGATCTTTGCTGCAAAAGGAGAAATTTGGCAAGGAATGATATATCATCAAGC 1758
Db 1802 TGCCCAACGACTATGTGCAAGAGGGGAGATCGGCGGTGAGATGTATCATCTCCAGG 1861
QY 1759 ATGGAAGTCCCAAGTTCTTGGAGCCCTGATGGTACTAAAGTTCTGGTTACTCTGAAAG 1818

Db 1862 CAGGCAAGTGCAGGTCTTGGCGGCCCTGATGGAAATCTGTGCTGGTGCACCTGAAAG 1921
QY 1819 CTGGGTGCTGTTTGGAGAAATCAGCTTCTAGCAGAGAGAGAGAAACCGTCGAACCTG 1878
Db 1922 CTGATCTGTTTGGAGAAATTAAGTCTGTGCTGCTTGTGGGGCGGGAACCGGCGACGG 1981
QY 1879 CCAATGTGGTGGCCACGGGTTTCCAAATCTTTAACTCTAGACAAAAGACCTCCAAAG 1938
Db 1982 CCAAGTGTGGCGACGGTTTACCACCTCTTCTATCTGATTAAGAGGACCTGAATG 2041
QY 1939 AAATTTCTAGTGCATTTATCAGATCTTGAAGGATCTCTATGAAGAAAGCCAGAGTCTTT 1998
Db 2042 AGATTTTGTGCTATTTCTGAGTCTCAGAAGTTACTCCGGAAGAAAGCCAGGCGATGC 2101
QY 1999 TAAAGCAGAGGCTAAGACCGCAGAG 2025
Db 2102 TGGAAGCAACATAAGCCCAAGAGG 2128

RESULT 2

US-10-159-563-147
; Sequence 147, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56USII
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 4382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-147

Query Match 21.4%; Score 577.4; DB 16; Length 4382;
Best Local Similarity 64.3%; Pred. No. 1.3e-118;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;
QY 679 TTCCAAACAGCATAGATTCATACACAGATCGACTCTATCTCTGTGGCTCTTGTGTC 738
Db 1983 TTCCCCAGAGCATTGACCCGCTGACCAACCTGATGATGCTATGCTGTCTTCTGG 2042
QY 739 CTCTTGCCCTATACTGGAACCTGCTGTTTATACCACTGGCGCTCGTCTTCCCATATAA 798
Db 2043 TGATGGCTCGAAATTTGGAACCTGTTGGCTGATTCGCTGGCTTCCCTTACCAGA 2102
QY 799 CCGCAGACAAACATACACTACTGCTTATTCGGGACATCATATGATATCATCTACCTTT 858
Db 2103 CCGGCAACATCCACCACTGGCTGCTGATGATTAACCTATGCGACCTCATCTACTTC 2162
QY 859 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTGAAGAGGAGAGACATAATAGTG 918
Db 2163 TGGACATCACCGTGTTCAGACACGCTGCACTTGTGTCAGAGCGGGGACATCATACGG 2222
QY 919 ATTCAATGAGCTAAGAAACACTACAGGACTTCTCAAAATTTCACTTGGATGTCGCAT 978
Db 2223 ACAAAAGGACATCGGAAATTAATCTAGTCTCGCGCTCAAGATGGACCTGCTCA 2282
QY 979 CAATAATACCATTTGATTTGTTGCTTCTTCTTGGGTTTAAATCCAAATTTTAGAGCAA 1038
Db 2283 GCCTCTCGCTTGGATTTCTCTATTGAAAGTCGGTGTGAACCCCTCTCCGCTGC 2342
QY 1039 ATAGGATGTTAAAGTACACTTCTTTTGAATTTAATCATCATCTAGCTATGATG 1098

Db 2343 CCCGCTGTTTAAAGTACATGGCTCTCTCGAGCTTTTAAACAGCGCGCTGGAATCCATCCTCA 2402
QY 1099 ACAAGCATATCTACAGAGTATTCGAACAACCTGGATCTTCTGCTTTTATCTGACACA 1158
Db 2403 GCAAGCCTACGTGTACAGGTCATCAGGACACACCTTACCTTCTTACAGCCTGCAAT 2462
QY 1159 TTAATCCCTGTGTTTATTACTGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGG 1218
Db 2463 TGAATTCCTGTCTTTATTACTGGCATCGCCTATCAGGGCTCGCTCCACTCACTGG 2522
QY 1219 TGTATGATGGGAGGAGAGTATCTCAGATGTTATTTATTTGGCAGTTTGAACCTTAA 1278
Db 2523 TTTACATGCGGTGGGAAACAGTTATTTCTGCTGTTTACTTCTGCTGGAAGACCTTCA 2582
QY 1279 TTACCATTTGGTGGCTTCCAGAACACAACTTTATTTGAATTTGTTTTCCTCACTTTGA 1338
Db 2583 TCACCATCGGGGCTGCTGCTGACCCCAAGACACCTCTTGAATTTGCTTCCAGCTGCTGA 2642
QY 1339 ATTTTCTTTCTGAGTTTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGATGATTG 1398
Db 2643 ATTATTTCAAGGCGTCTTTGCTTCTCTGTGATGATCGGACAGATGAGATGTTGTTAG 2702
QY 1399 GAGCAGCTACAGCAATCAGAACTACTTCCGGGCTGCTGATGATGACACACCTTGCCTACA 1458
Db 2703 GGGCCGCGCCGCGGACAGACCTACTACCGCAGCTGATGACAGCAGCGTGAAGTACA 2762
QY 1459 TGAACAATTTACTCCATTCTTAACTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATATA 1518
Db 2763 TGAATTTTACAAAGTCCCAAGTCGGTGCAGAACCGGTCAGAACCTGGTACAGTACA 2822
QY 1519 CATGGACTCTCAAGAAATGCTAGATGAGTCTGATTGCTTAAAGACCTTCACTCACTACGG 1578
Db 2823 CCTGGCAGCTCGAAGSCATCTGGATGATGATGATGATGATGATGATGATGATGATGATG 2882
QY 1579 TCCAGTTAGCCCTCGCATTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1638
Db 2883 TCGCGTGCAGCTCGCATTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2942
QY 1639 AGGTTGTGATACACAGATGATTTATGATGATGATGATGATGATGATGATGATGATGATG 1698
Db 2943 AGGCTGTGACCGGACAGATGATTTGATGATGATGATGATGATGATGATGATGATGATG 3002
QY 1699 TGGCTGGTGAATTTGTCGCAAAAGGAGAAATTTGGCAAGGAATGATGATGATGATGATGATG 1758
Db 3003 TGCCCAACAGCTATGTTGTCAGAAAGGGGAGATCGGCCGTGAGATGATGATGATGATGATG 3062
QY 1759 ATGGAGAGTCCAAAGTCTTGGAGGCGCTGATGATGATGATGATGATGATGATGATGATG 1818
Db 3063 CAGGCAAGTGCAGTCTTGGCGGCGCTGATGATGATGATGATGATGATGATGATGATGATG 3122
QY 1819 CTGGGTCGGTGTGAGAAATCAGCTTCTAGCAGAGGAGGAGAAACCGTGCAGACTG 1878
Db 3123 CTGGATCTGTGTTGGAGAAATAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3182
QY 1879 CCAATGTGTGGCCACGCGTTTGCATCTTTTAACTCTAGACAAAAGACCTTCCCAAG 1938
Db 3183 CCNACGTGTGGCGACGCGTTTCCACCTTCTCTGATGATGATGATGATGATGATGATGATG 3242
QY 1939 AAATTTCTAGTATTCAGATCTTGAAGATCTCTCATGAGAAAGCCAGATGTTT 1998
Db 3243 AGATTTTGTGATTTATCTGAGTCTCAGAGTTTACTCCGGAAGAAAGCCAGGCGCATGC 3302
QY 1999 TAAAGCAGAGGCTTAAGCCGACAGAG 2025
Db 3303 TGNAGACCAACAATAAGCCACAGGAGG 3329

RESULT 3

US-10-027-632-204539
; Sequence 204539, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204539
; LENGTH: 680
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(680)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-204539

Query Match 11.3%; Score 306; DB 13; Length 680;
Best Local Similarity 99.7%; Pred. No. 3.1e-58;
Matches 317; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2163 CAGAGAAAGAAAATTTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2222
Db 364 CAGAGAAAGAAAATTTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 423
QY 2223 AAAGAAATGAGATATACAAACAAAGAAATGAGATATGAGATATGAGATATGAGATATGAG 2282
Db 424 AAAGAAATGAGATATACAAACAAAGAAATGAGATATGAGATATGAGATATGAGATATGAG 483
QY 2283 GATAAGGAG 2342
Db 484 GATAAGGAG 543
QY 2343 ATTGCAGTGGAG 2402
Db 544 ATTGCAGTGGAG 603
QY 2403 CGTCAATCACTCATTTATCAGCATGGCTCTCTCTGCTGAGGCGGAGAGAGAGAGAGAG 2462
Db 604 CGTCAATCACTCATTTATCAGCATGGCTCTCTCTGCTGAGGCGGAGAGAGAGAGAGAG 663
QY 2463 ATTGAAGTCAAGAAAG 2480
Db 664 A-TGAAGTCAAGAAAG 680

RESULT 4

US-10-027-632-204539
; Sequence 204539, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12


```

Db      862  TTCACCGGCTACTGAGTTTCCGGCTCTTTGAAATCTTTGACCGCAGAGACAAGG 921
QY      1095  ATGGCAAAAGCATATATCTACAGAGTTATTCGAACAACCTGGATATCTGTTTATCTG 1154
Db      922  ACCAATACCCCAATATGTTCAAGATTGGAACTTGGTCTTGATATCTCATCATCATC 981
QY      1155  CACATTAATGCTGTTTATTTACTGGGCTTCAAACTATGAAGAAATGGCACTACTAGA 1214
Db      982  CACTGGAATGCTGCTGATCTACTTTGCGCATTCCTCAAGTTTCATGTTTGGGACAGCTCC 1041
QY      1215  TGGGTGT-----ATGATGGGGAAGAAACGAGTATCTGAGA 1250
Db      1042  TGGGTCTACCCAAACATCTCAATCCAGAGCATGGCGCTCTCCAGGAATGACATTTAC 1101
QY      1251  TGTATATATGGGAGTTCGAATTAATACCATTTGTTGGCTTCGAGAACCAAACT 1310
Db      1102  AGTCTCTACTGCTCCACCTTGACCTTACCACTTGGTGGAGACCCACCCCGTGAAA 1161
QY      1311  TTATTTGAAATTTGTTTCAACTCTGAATTTTCTGGAGTTTCTGAGTTCTCCAGT 1370
Db      1162  GATGAGGATCTCTTTGCTGCTAGACTTCTTGGTGGTGTCTGATTTTGGCCACC 1221
QY      1371  TTAATTTGTCAGATGAGAGATGTGATTTGGAGCAGCTACAGCCAAATCAGAACTACTTCGGC 1430
Db      1222  ATTGTGGGCAATGTGGGCTCCATGATCTCGAATATGAATGCTCAGCGGCAGAGTTCCAG 1281
QY      1431  GCTCCTCATGATGACACCAATTCCTTACATGATTAATCTCCATCTCTTAACTTTGTGCAA 1490
Db      1282  GCCAAGATGATTCCTCAGCAGTACATGATCTCGAATGATGATTCGCAAGGATCAACAGGACTTGGAG 1341
QY      1491  AAGCGAGTTCGAGCTTGTATGAATATATACATGGGACTCTCAAGAAATGTAGATGAGTCT 1550
Db      1342  ACGCGGTTATCCGGTGTGTTGACTACCTGTGGGCAACAAAGAGACGGTGTGATGAGAAG 1401
QY      1551  GATTTGCTTAAGACCTACCACTACGCTCAGTTAGCCCTCGGCATGATGATGAACTTC 1610
Db      1402  GAGTGTCTCAAGAGCTCCAGAGCAAGCTGAAGCTGAGATTCGCAAGCTCAACGTCACCTG 1461
QY      1611  AGCATCATCAGCAAGTGCATCTGTTCAAGGGTGTGTATACACAGATGATTTATGACATG 1670
Db      1462  GACAGCTGAAGAGTTGCGATCTTCCAGACTGTGAGGACGGCTGCTGTTGGAGCTG 1521
QY      1671  TTGCTAAGATTAATTCGGTCTCTATTTGCTGGTGTGATTTGCTGCAAAAAGGGAGAA 1730
Db      1522  GTGCTGAAGCTGCGACCCACTGTGTTGAGCCCTGGGATTTATATCTGCAAGAGGGAGAT 1581
QY      1731  ATTGGCAAGAAATGTATATCATCAAGCATGAGAGTCCAAAGTCTTGGAGGCCCTGAT 1790
Db      1582  ATTGGGAAGAGATGTACATCATCAAGAGGGCAAGCTGGCGGTGGTGGCTGATGATGGG 1641
QY      1791  GGTACTAAAGTTCTGGTTACTCTGAAAGCTGGGTCGGTGTGTTGGAGAAATCAGCCCTTCT- 1849
Db      1642  GTCACCCAGTTTCGTGGT---CCTCAGCGATGGCAGCTACTTTCGGGAGATCAGCAATTCG 1698
QY      1850  AGCAGCAGGAGGAGGAAACGTCGCAACTGC 1879
Db      1699  AACATCAAGGGAGCAAGTCTGGGNAACCGC 1728

```

RESULT 10
 US-10-087-217-1
 ; Sequence 1, Application US/10087217
 ; Publication No. US20030100059A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aptus Genomics, Inc.
 ; APPLICANT: YAO, Yong
 ; APPLICANT: CAO, Liang
 ; TITLE OF INVENTION: No. US20030100059A1 Cell-Based Assays for G-Protein-Coupled Receptors
 ; TITLE OF INVENTION: Activities
 ; FILE REFERENCE: 53735-5004-US
 ; CURRENT APPLICATION NUMBER: US/10/087,217
 ; CURRENT FILING DATE: 2002-03-04

```

; PRIOR APPLICATION NUMBER: 60/330,663
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1992)
; OTHER INFORMATION:
US-10-087-217-1

```

Query Match 4.9%; Score 131.6; DB 15; Length 1995;
 Best Local Similarity 46.7%; Pred. No. 6.8e-19;
 Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;

```

QY      714  TATCTCTGTGGCTCTGCTTGCCTCTTGCCTATACCTGGAACCTGGTTTATACCA 773
Db      424  TATACCGTTGGTGTGTTGTCATTCGCATGCTCTTCAACACTGGTGCCTGTGGTG 483
QY      774  CTGCGCTCTGCTTCCCATATCAAAACCGCAGACAACATACACTACTGGCTTATTCGGAC 833
Db      484  GCCAGAGCTGCTTCACTGATCTACAGAGAACTATTTGTGATGCTGCTGCTGGAC 543
QY      834  ATCATATGTATATCATCTTACCTTTATGATGATGCTATTTATCCAGCCAGACTCCAGTTT 893
Db      544  TACTTCTCAGACACTGTCTATATCGAGACCTCATCATTCGGCTCGCACAGGC---TTC 600
QY      894  GTAAGAGGAGGAGACATATAGTGAATCAAAATAGCTAAGGAAACACTACAGGACTTCT 953
Db      601  CTAGAACAGGGCTCTTGTCTCAAGATCCAGAAATTCGAGACAATATATACACT 660
QY      954  ACAAAATTCAGTTGGATGTCGATCAATAATACCATTTGATTTATTTGCTACTCTTCTTT 1013
Db      661  TTGCAAGTTCAAAATGGATGTGCTCTATCATTCCTCCACTGACCTTATCTATTTGCTGTG 720
QY      1014  GGGTT---TAATCCAATGTTTAGACAAATAGGATGTTAAAGTACACATTCATTTTGA 1070
Db      721  GGTATCCACAGCCCTGAGGATGCTTCAACCGTCTATTTACACTTTGCCCGTATGTTGAG 780
QY      1071  TTTAATCATACCTAGATCTATATAGGACAAAGCATATATCTACAGAGTTATTCGAACA 1130
Db      781  TTCTTTGACCGCACTGAGACAGCACAGTACCCCAACATCTCCGAATCAGCAATCTG 840
QY      1131  ACTGGTACTTCTGTTTATTTCTGCACATTAATGCTGCTGTTTATTTACTGGCTTCAAC 1190
Db      841  GTCCCTTTACATCTTGGTCATCATCCACTGGAATGCTGTATTTATTTATTTCTTAAG 900
QY      1191  TATGAAGGAATGG-----CACTACTAGATGGGTGTATGAT 1226
Db      901  TCCATTGGCTTGGAGTTGACACCTGGGTTTACCCCAACATTTACTGACCTGATATGGC 960
QY      1227  GGGGAGGAAACAGATATCTGAGATGTTTATTTGGGCAAGTTTCAACTTTAATTTACCAT 1286
Db      961  TACCTGGCTAGAGATACATTTACTGCTTTTACTGGTCCACACTGACCCCTCACCCACT 1020
QY      1287  GGTGGCTTCCAGAACCAACAACTTTATTTGAAATTTGTTTTTCAACTCTTGAATTTTTT 1346
Db      1021  GGAGAGACACACCCCTGTAAAGGATGAGGATACCTATTTGTCACTTTTGACTTTTG 1080
QY      1347  TCTGGAGTTTGTGTTCTCCAGTTTAAATGCTCAGATGAGAGATGTTGATTTGGAGAGCT 1406
Db      1081  ATTGGTGTCTCATCTTTGCCACTATTGTGGGAAATGTGGGCTCCATGATCTCCAAACATG 1140
QY      1407  ACAGCCAATCAGAACTACTTCCGCGCTGATGATGACACCACTTGGCTCATCAACAAT 1466
Db      1141  AATSCCAGCAGCAGAGTTCCAGGCCAAGATTGATGCTGTCAAACTACTAGTGCAGTTC 1200
QY      1467  TACTCCATTCCTAACTTTGTGCAAAAGCGAGTTGCGACTTGGTATGAAATATACATGGGAC 1526
Db      1201  CGAAAGGTGAGAAAGAGATGGAAGCAAGGTGATCAAAATGGTTTGGACTACTTGTGGACC 1260

```

QY 1527 TCTCAAGATGCTAGATAGTCTGATTGCTTAAAGACCTACCACTACGGTCCAGTTA 1586
Db 1261 AATAAGAGACAGTAGAAGACGAGAGAGTCTCCAGAACCTGCCAAGACTCAGGGCT 1320
QY 1587 GCCTCGCCATTGATGTAACCTTACAGATCATCAGCAAGAGTGCATGTTCAAGGGTTGT 1646
Db 1321 GAGATAGCCATTAAATGTTCACTTGTCCACTCTGAAGAAAGTGGCATAITCCAGGATTGT 1380
QY 1647 GATACACAGATGATTTATGACATGTTGCTTAAGATTGAATCCCTTCTATTTGCCCTGGT 1706
Db 1381 GAAGCTGGCTACTGGTGGAACTGGTACTGAAGCTTCGCTCAGGTCTTTAGTCTCTGGA 1440
QY 1707 GACTTTCTGTCGAAAAGGAGAGAAATGGCAAGGAAATGTATATCATCAAGCATGAGAGAA 1766
Db 1441 GATTATATTTGCCGTAAGGGGACATTTGGCAAGGAAATGTATCATCATCAAGGAGGCAAG 1500
QY 1767 GTCCAAAGTTCTTGAGGCCCTGATGGTACTAAAGTTCTGGT----TACTCTGAAGCTGG 1822
Db 1501 TTGGCAGTGGTAGCTGATGATGGCGTGACTCAGTATGCGCTTGCTCTCAGCTGGGAGCTGC 1560
QY 1823 GTGGCTGTTTGGGAAATCAGCCTTCTAGCAGCAGGAGGA--GGAAACCGTCCGAAGCTGCC 1880
Db 1561 TTGGTGAGATTAGTATCTTACATTTAAGGTAGCAAAATGGCAATCGACGTACTGCT 1620
QY 1881 AATGCTGGCCCGGTTGGCAATCTTTTAACTCTAGACAAAAGACCCCTCCAGAA 1940
Db 1621 AATATCGTAGCTGGGCTACTCAGATCTCTTCTGCTTGTCGAAGCAGATCTTATGGAA 1680
QY 1941 ATTCTAGTATATCAGATCTTGAAGGATCCTCATGAAGAAAGCAGAGTCTTTTA 2000
Db 1681 GCTGTACTAGTATCTGTATGCCAAGAGTCTCTGGAGAACGGGGTAGGAGATCCTG 1740
QY 2001 AAGCAGAAGGCT 2012
Db 1741 ATGAAGGAGGT 1752

RESULT 11
US-10-087-217-5
; Sequence 5, Application US/10087217
; Publication No. US20030100059A1
; GENERAL INFORMATION:
; APPLICANT: Aptus Genomics, Inc.
; APPLICANT: YAO, fong
; TITLE OF INVENTION: Cell-Based Assays for G-Protein-Coupled Receptors
; TITLE OF INVENTION: Activities
; FILE REFERENCE: 53735-5004-US
; CURRENT APPLICATION NUMBER: US/10/087,217
; PRIOR FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1992)
; OTHER INFORMATION:
US-10-087-217-5

Query Match 4.9%; Score 131.6; DB 15; Length 1995;
Best Local Similarity 46.7%; Pred. No. 6.8e-19;
Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;
QY 714 TATCTCCGTGGCTCTGCTGTCATCTTGCCTATAACTGGAAGTCTGCTGTTTATACCA 773
Db 424 TATTAACCGTTGGTCTGTTGTCATTCCTCCATGCTGTTCTTTACAACTGGTGGCTGTTGGTG 483

QY 774 CTGGCCCTGCTTCCCATATCAAAACCGCAGCAACATACACTACTGGCTTATTTGGGAC 833
Db 484 GCCAGAGCCTGCTTCAAGTATCTACAGAGAACTATTTTGGTATGGCTGGTGGAC 543
QY 834 ATCATATGATATCATCTACTTATGATATGATATTTATCCAGCCAGACTCCAGTT 893
Db 544 TACTTCTCAGACATGCTTATATCGACACTCATCATTCGGCTGGCAGAGC---TTC 600
QY 894 GTAAGAGGAGGAGACATATATAGTGATTCAAATAGCTTAAGGAACTACAGAGACTCT 953
Db 601 CTAGAACAAGGGCTCTTGGTCAAGATCCCAAGAAATTCGAGACAACTATATTCACT 660
QY 954 ACAAAATTTCAAGTTGATGTCGCATCATATACATTTGATATTTGCTACTCTTCTTT 1013
Db 661 TTGCAAGTTCAAAATGGATGGCTTCTATCATTCCTCAGCTGATCTATTTTCTGCTGG 720
QY 1014 GGGTT---TAATCCAAATGTTTAGAGCAATAGGATGTTAAAGTACACTTCAATTTTGA 1070
Db 721 GGTATCCACAGCCCTGAGTAGCTTCAACGCTCTATTACACTTTGCCCGTATGTTGAG 780
QY 1071 TTTAATCATCATCCTAGAGTCTATTAATGGACAAAGATATCTACAGAGTTATTCGAACA 1130
Db 781 TTCTTTGACCGCACTGAGACACGCAACCACTCTCCGAATCAGCAATCTG 840
QY 1131 ACTGGATCTTCTGTTTATCTGCACATTAATGCTGTTTATTTACTGGGCTTCAAA 1190
Db 841 GTCTTTTACATCTTGGTCACTCCACTGGAATGCTTGTATTTATGTTATTTCTAAG 900
QY 1191 TATGAAGGAATGG-----CACTACTAGATGGGTGTATGAT 1226
Db 901 TCCATTGGCTTTGGAGTTGACACCTGGGTTTACCCTCAACATTTACTGACCTGAATATGGC 960
QY 1227 GGGGAAGGAAACGATATCTGAGATGTTATTTGGCAGTTGCGAATTTAATTAACCAT 1286
Db 961 TACCTGGCTAGAGATACATTTACTGCTTTACTGGTCCACACTGACCTCACCACAT 1020
QY 1287 GGTGGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTTTCACTCTGTAATTTTTT 1346
Db 1021 GGAGAGACACACCCCTGTAAGGATGAGGATACCTATTGTCATCTTTGACTTCTTG 1080
QY 1347 TCTGGAGTTTTGTTCTTCCAGTTTAAATTTGTCAGATGAGAGATGTTGATGAGCAGT 1406
Db 1081 ATTGGTGTCTCATCTTTGCCACTATTTGGGAAATGTTGGGCTCCATGATCTCCAACTG 1140
QY 1407 ACAGGCAATCAGAACTACTTCCGCTGCTATGAGTACACCATTCCTTACATGAACAT 1466
Db 1141 AATGCCACAGCAGCAGAGTTCCAGCCAGATTTGATGCTGCAACACTACATGCGATTC 1200
QY 1467 TACTCCATTTCTTAAACTTGTGCAAAAGCGAGTTGCGACTTTGGTATGAATATACATGGGAC 1526
Db 1201 CGAAAGGTGAGCAAGACATGGAAGCCAAAGTTCATCAATGTTTGGTACTTTGGGACC 1260
QY 1527 TCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAGACCTTACCACTACGGTCCAGTTA 1586
Db 1261 AATAAGAACAGCTAGTAGAAGCTTCCAAAGAACCTGCGCAAGAGCTCAGGGCT 1320
QY 1587 GCCTCGCCATTTGATGTAACCTTCAAGCATCATCAGCAAAAGTGCATTTGTTCAAGGGTTGT 1646
Db 1321 GAGATAGCCATTAAATGTTCACTTGTCCACTCTGAAGAAAGTGGCATAITTCAGGATTGG 1380
QY 1647 GATACACAGATGATTTATGACATGTTGCTAAGATTGAATTCGTTCTTATTTGCCCTGGT 1706
Db 1381 GAAGCTGGCTTACTGCTGGAACCTGGTACTGGAAGCTTCGCTCAGGTCTTTAGTCTCTGGA 1440
QY 1707 GACTTTTCTGCAAAAGGAGAGAAATTTGGCAAGGAAATGTATATCATCAAGCATGAGAGAA 1766
Db 1441 GATTATATTTGCCGTAAGGGGACATTTGCAGGAAATGTATCATCATCAAGGAGGCAAG 1500
QY 1767 GTCCAAAGTTCTTGAGGCCCTGATGATGTAATAAGTTCTGGT----TACTCTGAAGCTGG 1822
Db 1501 TTGGCAGTGGTAGCTGATGATGGCGTGACTCAGTATGCGCTTGTCTCAGCTGGAGCTGC 1560
QY 1823 GTGGCTTGGGAGAAATCAGCCTTCTAGCAGCAGGAGGA--GGAAACCGTCCGAAGCTGCC 1880

Db 1561 TTTGGTGGAGTAGTATCTCTTAACATTAAGGGTAGCAAAATGGGCAATGCGACTACTGCT 1620
QY 1881 AATGTGGTGGCCACGGGTTTCCCAATCTTTTAACTCTAGACAAAGACCCCTCCAAGAA 1940
Db 1621 AATATCCGTAGCTGGGCTACTCAGATCTCTTCTGTTTCAAGGACGATCTTATGGAA 1680
QY 1941 ATTCTAGTCATATCCAGATTTCTGAAGGATCTCTATGAAGAACCCAGAGTGTCTTTTA 2000
Db 1681 GCTGTAACATGAGTATCTCTGATGCCAAGAGGTCCTGGAGGAACGGGGTAGGAGATCCTG 1740
QY 2001 AAGCAGAGGCT 2012
Db 1741 ATGAAGATGGGT 1752

RESULT 12
US-10-295-573-2
; Sequence 2, Application US/10295573
; Publication No. US2003015751A1
; GENERAL INFORMATION:
; APPLICANT: Karpen, Jeffrey W.
; APPLICANT: Rich, Thomas C.
; APPLICANT: Cooper, Dermot M.F.
; APPLICANT: Schack, Jerome
; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS
; FILE REFERENCE: UTC-07536
; CURRENT APPLICATION NUMBER: US/10/295,573
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/332,494
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 3027
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-295-573-2

Query Match 4.9%; Score 131.6; DB 15; Length 3027;
Best Local Similarity 46.7%; Pred. No. 8.5e-19;
Matches 622; Conservative 0; Mismatches 674; Indels 36; Gaps 5;

QY 714 TATCTCTGCTGCTTCTGCTTGTCTCACTCTTCCCTATAAAGTGAAGTCTGCTTTATACCA 773
Db 763 TATTACCGCTGCTTGTGTTGTTGCTCAATGCCATGCTGTTCTTTACAACTGGTGGCTGGTG 822
QY 774 CTGGCCCTGCTTCCCATATCAACCCGACAGACATACACTACTGCTTATGGGAC 833
Db 823 GCCAGAGCTGCTTCAAGTATCTACAGAGAACTATTTTGGTATGGCTGGTGGTGGAC 882
QY 834 ATCATATGTATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTT 893
Db 883 TACTTCTCAGACACTGTCTATATCGCAGACCTCATCTCGGCTGGCAGAGC---TTC 939
QY 894 GTAAGAGAGAGACATATAGTGGATTCATAGAGCTTAAGAACTACAGAGACTTCT 953
Db 940 CTGAACAGGGGCTCTTGGTCAAGATCCCAAGAAATTTGGAGACAACTATATTCACACT 999
QY 954 ACAAAATTCAGTTGGATGTCGCATCAATATACATTTGATATTTGCTACCTCTCTTT 1013
Db 1000 TTGCAGTTCAATTTGGATGGCTTCTATCTATCCCACTGACCTTATCTATTTGGTG 1059
QY 1014 GGGT---TAATCAATGTTTAGAGCAATAGGATGTTAAAGTACATCTTCAATTTTGA 1070
Db 1060 GGATATCCACAGCCCTGAGGTACGCTTCAACCGCTTATACACTTTGCCCGTATGTTGAG 1119
QY 1071 TTTAATCATCATCTAGAGTCTATATGGAACAAGCATATATCTACAGATTTTCGAACA 1130
Db 1120 TTTCTTACCCGCTAGAGACAGCAGCAGCTACCCCAACATCTCCGAATCAGCAATCTG 1179
QY 1131 ACTGGATACATGCTGTTGTTTATCTGCAATTAATGCTGTTTATCTACTGGGCTTCAAC 1190

Db 1180 GTCCCTTTACATCTTGTGTCATCATCCACTGGAATGCTTGTATTATTATTATTTTCTAAG 1239
QY 1191 TATCAAGGAATTTGG-----CACTACTAGATGGGTGTATGAT 1226
Db 1240 TCCATTTGGCTTTGGAGTTGACACCTTGGGTTTACCCCAACATTACTGACCCCTGAATATGGC 1299
QY 1227 GGGGAAGGAAACAGATATCTGAGATGTTTATTATTGGGAGTTTGGAGTTCGAACCTTTAATTTACCATT 1286
Db 1300 TACTCGCTAGAGAGTACATTTACTGTCTTTTACTGTCTTCCACACTGACCCCTCAACCCATT 1359
QY 1287 GGTGGCTTCCAGAACCAACAACTTTTATTGAAATTTGTTTTTCAACTCTTGAATTTTTT 1346
Db 1360 GGAGAGACACCCCTCTTAAGGATGAGGAGTACCTTATTGTCATCTTTGACTTTCTTG 1419
QY 1347 TCTGAGTTTTTGTGTTCTCCAGTTTAAATTGGTTCAGATGAGAGATGTTGATTTGAGCAGCT 1406
Db 1420 ATTGGTGTCTCATCTTTGCCACTATTGTTGGAAATGTTGGGCTCCATGATCTCCAACATG 1479
QY 1407 ACAGCCAATCAGAACTACTTCCGCCCTGCATGGATGACACCACTTGCCTACATGACAAAT 1466
Db 1480 AATGCCACAGCAGAGATTTCCAGGCCAAGATTGATGTGTCAAAACACTTACATGCAATTC 1539
QY 1467 TACTCCATTCTAAACTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATATACATGGGAC 1526
Db 1540 CGAAAGGTGAGCAAGACATGGAAGCCAAAGGTCATCAATGTTGTTGACTTACTTTGGACC 1599
QY 1527 TCTCAAGATGCTAGATGATGCTGATTTGCTTAAGACCTTACCACTACGCTCCAGTTA 1586
Db 1600 AATAAGAGACAGTATGATGAACGAGAAGTCTTCAAGAACCTGCCAGCAAGCTCAGGCT 1659
QY 1587 GCCTCGCAATGATGTGAACCTTCCAGCATCATCAGCAAGTCGACTTGTTCAGAGGTTGT 1646
Db 1660 GAGATAGCCATTAAATGTTTCCACTCTGAAGAAAGTGGCATATTTCCAGGATTTG 1719
QY 1647 GATACAGATGATTTATGACATGTTGCTAAGATTGAATTCGTTCTCTATTGCTGCT 1706
Db 1720 GAAGCTGGCTTACTGTGGAACTGGTACTGAACTTCGCTCTCAGGTTCTTTAGTCTTGA 1779
QY 1707 GACTTTGTCTCAAAAGGGAGAAATTTGCAAGGAAATGATATCATCAAGCATGGAGAA 1766
Db 1780 GATTATATTTGGCTTAGGGGACATTTGGCAAGGAAATGATCATCATCAAGAGGGCAAG 1839
QY 1767 GTCCAGTTCTTGGAGGCCCTGATGTTACTAAAGTTCTGGT----TACTCTGAAGCTGG 1822
Db 1840 TTGGCAGTGGTACGTGATGCTGCTGACTCAGTATGCTTGTCTCAGCTGGAGCTGC 1899
QY 1823 GTCCGTGTTTGGAGAAATCAGCTTCTAGCAGCAGGAGGA--GGAAACGCTGCACTGCC 1880
Db 1900 TTTGGTGAATTAGTATCTTAAATTAAGGTAGCAAAATGGGCAATCGACGACTGCT 1959
QY 1881 AATGTGTGGCCCGGCTTTGCCAATCTTTTAACTCTAGACAAAGACCCCTCCAAGAA 1940
Db 1960 AATATCCGTAGCTGGGCTACTCAGATCTCTTCTGCTTGTCCAGGACGATCTTATGAA 2019
QY 1941 ATTCTAGTCATATCCAGATTTCTGAAGGATCTCTCATGAAGAAAGCCAGAGTGTCTTTA 2000
Db 2020 GCTGTAACATGAGTATCTCTGATGCCAAGAGGTCCTGGAGGAACGGGGTAGGAGATCCTG 2079
QY 2001 AAGCAGAGGCT 2012
Db 2080 ATGAAGATGGGT 2091

RESULT 13
US-10-295-573-4
; Sequence 4, Application US/10295573
; Publication No. US2003015751A1
; GENERAL INFORMATION:
; APPLICANT: Karpen, Jeffrey W.
; APPLICANT: Rich, Thomas C.
; APPLICANT: Cooper, Dermot M.F.
; APPLICANT: Schack, Jerome
; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS


```

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 12975
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013751.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.65
; US-09-864-761-12975

Query Match
Best Local Similarity 4.8%; Score 129; DB 9; Length 526;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 AGACAACTCTCCAGAGAAATTCCTCTGGAGATCTGACCAAAACCCCTGACCCCTCAAAA 331
DB 191 AGACAACTCTCCAGAGAAATTCCTCTGGAGATCTGACCAAAACCCCTGACCCCTCAAAA 250

QY 332 TGCAGCAGAACCAACTGCAAGTGCAGAGCAGAGCAAGAAATGACCCCGGGAAGAGG 391
DB 251 TGCAGCAGAACCAACTGCAAGTGCAGAGCAGAGCAAGAAATGACCCCGGGAAGAGG 310

QY 392 TCCAAACAG 400
DB 311 TCCAAACAG 319

RESULT 15
US-10-087-217-3
; Sequence 3, Application US/10087217
; Publication No. US20030100059A1
; GENERAL INFORMATION:
; APPLICANT: Aptus Genomics, Inc.
; APPLICANT: YAO, Yong
; APPLICANT: CAO, Liang
; TITLE OF INVENTION: No. US20030100059A1 Cell-Based Assays for G-Protein-Coupled Receptors
; FILE REFERENCE: 53735-5004-US
; CURRENT APPLICATION NUMBER: US/10/087,217
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: 60/330,663
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1992)
; OTHER INFORMATION:
; US-10-087-217-3

```

```

Query Match
Best Local Similarity 4.8%; Score 128.4; DB 15; Length 1995;
Matches 620; Conservative 0; Mismatches 676; Indels 36; Gaps 5;

QY 714 TATCTCCTGTGGCTCTTGTCTGTGTCACTTGTGCTATAAAGTGAACCTGCTGGTTATACCA 773
DB 424 TATTACCGTTGGTTGTTTGTCACTTGTGCTATAAAGTGAACCTGCTGGTTATACCA 483

QY 774 CTGGGCTGTCTTCCCATATCAACCGGAGACAACATACACTATGCGCTTATTCGGGAC 833
DB 484 GCCAGAGCCTGTCTAGTATCTACAGAGAACTATTTTGTGTATGCGCTGCGGAC 543

QY 834 ATCATATGTATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTT 893
DB 544 TACTTCTCAGACACTGTCTATATCGCAGACCTCATCTTCGCTGCGGACAGGC---TTC 600

QY 894 GTAAGAGGAGAGACATAATAGTGATTCAAATAGAGTAAAGAAACACTACAGGACTTCT 953
DB 601 CTAGAACAGGGGCTCTTGTCTCAAGATCCCAAGAAATTCGAGACACTATATTCACACT 660

QY 954 ACAAAATTTTCACTGTGATGTCATCAATAATACCAATTTGATATTTGCTACCTCTCTTT 1013
DB 661 TTGCAGTTCAAAATGATGCTGCTTCTATCATTCACACTGACCTTATCTATTTGCTGTG 720

QY 1014 GGGTT---TAATCCAAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCAATTTTGA 1070
DB 721 GGTATCCACAGCCCTGAGGTACGCTTCAACCGTCTATTACACTTTGCCCGCTATTGTTG 780

QY 1071 TTTAATCATCACTAGAGTCTATAATGCAAGACATATATCTACAGAGTATTTCGAACA 1130
DB 781 TTCTTTGACCGCACTGAGACAGCACCAGCTACCCCAACATCTTCGAAATCAGCAATCTG 840

QY 1131 ACTGGATCTTCTGCTTTTATCTGCACATTAATGCTGTGTTTATTTACTGGCTTCAAC 1190
DB 841 GTCTTTTACATCTTGTCTCATCATCCACTGGAATGCTTGTATTTATTTATTTCTTAAG 900

QY 1191 TATGAAGAAATGG-----CACTACTAGATGGGTGTATGAT 1226
DB 901 TCCATGCTTGGAGTTGACACCTGGGTTTACCCCAACATTTACTGACCTTGAATATGGC 960

QY 1227 GGGGAAGAAACAGGATCTCGAGATGTTTATTTATTTGGGAGTTCGAACCTTTAATTTACCAT 1286
DB 961 TACCTGGCTAGAGATGATTTACTGCTTTTCTGTTCCACACTGACCTCACCACCAT 1020

QY 1287 GGTGCTTCCAGAACCAAACTTTTGAATTTGTTTCAACTCTTGAATTTT 1346
DB 1021 GGAGAGACACCCCTGTTAAGGATGAGGATACCTATTGTGTCATCTTTGACTTCTTG 1080

QY 1347 TCTGAGTTTGTGTTCTCCAGTTTAAATGGTCCAGATGAGAGATGATGGAGCAGCT 1406
DB 1081 ATTGGTCTCTCATCTTTGCCACTATTGTTGGAAATGTTGGCTCCATGATCTCCAAATG 1140

QY 1407 ACAGCAATCAGAACTACTTCCGCGCTGTCATGGATGACACCACTTGTCTACATGAACAAT 1466
DB 1141 AATGCCACAGCAGAGTTCAGGCAAGATGATGCTGTCAACACTACATGCACTTC 1200

QY 1467 TACTCCATCTTAACTGTGCAAAACGAGTTGCGGACTTGGTATGATATACATGGGAC 1526
DB 1201 CGAAAGTTCAGCAAGACATGGAAGCCCAAGTCAATCAATGGTTGACTACTTGTGGACC 1260

QY 1527 TCTCAAGAATGCTAGATGATGTTGTTTGAAGACCTTCAACTACGCTCCAGTTA 1586
DB 1261 AATAAGAGCAGTAGATGAACGAGAGTCTCTCAAGACTGCGCAAGACTCAGGGCT 1320

QY 1587 GCCCTCGCATTTGATGAACTTCAGCATCATCAGCAAACTGCACTTGTTCAGGGTTGT 1646
DB 1321 GAGATAGCCATTAATGTTCACTTGTCCACTCTCAAGAAAGTGGCATATTTCCAGGATGT 1380

QY 1647 GATACACAGATGATTTATGACATGTTGCTAAGATTTGAATTCCTCTCTATTTGCTGCT 1706
DB 1381 GAAGTGGCCTACTGTTGGAACCTGCTAGCACTTGCCTCAGGCTTTTAGTCTCTGA 1440

QY 1707 GACTTTGCTGCAAAAGGAGAAATTTGGCAAGAAATGTATATCATCAAGCATGGAGAA 1766

```


Db 1441 GATTATATTTCCTAAGGGGACATTGGCAAGGAAATGTACATCATCAAGGAGGGCAAG 1500
QY 1767 GTCCAAAGTTCTTGGAGGCCCTGATGTACTAAAGTTCTGGT----TACTCTGAAAGCTGG 1822
Db 1501 TTGGCAGTGGTAGCTGATGATGGCGTGACTCAGTATGCCCTTGCTCTCAGCTGGGAGCTGC 1560
QY 1823 GTGGGTGTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGA--GGAAACCGTCGAACTGCC 1880
Db 1561 TTTGGTGAGATTAGTATCTTAAACATTAAAGGTTAGCAAAATGGGCAATCGACGTACTGCT 1620
QY 1881 AATGTGTGGCCCAAGGGGTTTGGCAATCTTTTAACTCTAGACAAAGACCCCTCCAAGAA 1940
Db 1621 AATATCCGTAGCCTGGGCTACTCAGATCTCTTCTGCTGTCCAAAGGACGATCTTATGGA 1680
QY 1941 ATTCTAGTGCATTAATCCAGATCTGAAAGGATCTCTCATGAGAAAGCCAGAGTGCCTTTA 2000
Db 1681 GCTGTAACTGAGGCTCTGTATGCCAAGAGGTCCTGGAGGAACGGGGTAGGAGATCCTG 1740
QY 2001 AAGCAGAGGCT 2012
Db 1741 ATGAAGGAAGT 1752

Search completed: June 22, 2004, 09:37:11
Job time : 1120.37 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 17:15:34 ; Search time 9321.39 Seconds
(without alignments)
11299.126 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 agctttaatcgtgcacaaa.....aagaaaagcgttaagcaataa 2430

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2430	100.0	4369	9	AF272900	Homo sapi
2	2049.4	84.3	2135	9	AF228520	Homo sapi
3	1689.2	69.2	2826	4	AF490511	Canis fam
4	1362.4	56.1	4710	10	MMU243572	Mus muscu
5	577.4	23.8	3025	9	HUMCNCCC	Homo sapien
6	577.4	23.8	3408	9	HUMCNCCC	Homo sapien
7	577.4	23.8	4033	9	HUSU5837	Human CGMP-
8	577.4	23.8	4382	9	AF042498	Homo sapi
9	575.2	23.7	4763	10	BC045114	Mus muscu
10	572.2	23.5	3083	4	AF074012	Bos tauru
11	572.2	23.5	3090	4	AF074013	Bos tauru
12	572.2	23.5	3253	4	BTCN34CGN	B. taurus mR
13	572.2	23.5	3290	4	AF074014	Bos tauru
14	572.2	23.5	4282	4	BTRPCNGCL	B. taurus mR
15	569.6	23.4	4238	10	RNCNG41	Rattus no
16	568	23.4	4236	10	RNCNG43	Rattus no
17	568	23.4	4236	10	RNCNG43	Rattus no
18	330	13.6	205816	9	AC013751	Homo sapi
19	237.4	9.8	2511	3	CEU73476	Caenorhadi
20	223	9.2	3358	3	BT001439	Drosophill
21	217.8	9.0	3099	10	BC046523	Mus muscu
22	196.2	8.1	441	10	AF015728	Rattus no
23	187.4	7.7	1709	3	AY060725	Drosophill
24	181.2	7.5	2061	4	SUS85404	Sus scrofa
25	181.2	7.5	2857	9	S42457	CNGG=rod ph
26	176.8	7.3	2697	4	CFACGMP	X99914 C.familiari
27	176.8	7.3	2717	4	CFU83305	U83905 Canis fam
28	176.4	7.3	2500	9	HUMCGMP	M84741 Human CGMP-
29	173.6	7.1	2682	4	BTCGMPCH	X51604 B.taurus RN
30	169.8	7.0	1874	9	AF547222	Homo sapi
31	169.8	7.0	181804	9	AC107068	Homo sapi
32	166.4	6.8	2297	10	MMU19717	Mus musculu
33	164.8	6.8	2474	10	MMDCNCG	M84742 Mus musculu
34	162.4	6.7	6312	3	AF091302	AF091302 Limulus p
35	161.4	6.6	58409	10	AL772281	Mouse DNA
36	155.6	6.4	2612	5	GGRODCNG	X89599 G.gallus mR
37	152	6.3	2052	10	RNU48803	U48803 Rattus norv
38	150.6	6.2	200535	10	AL671880	AL671880 Mouse DNA
39	150.6	6.2	222330	2	AC099698	AC099698 Mus muscu
40	150.2	6.2	181805	2	AC114445	AC114445 Rattus no
41	150.2	6.2	190000	2	AC007704	AC007704 Homo sapi
42	150.2	6.2	233700	2	AC117107	AC117107 Rattus no
43	150.2	6.2	274011	2	AC096142	AC096142 Rattus no
44	148.8	6.1	2148	10	RNU93851	U93851 Rattus norv
45	139.6	5.7	2049	5	ICTCNC	M83111 Ictalurus p

ALIGNMENTS

RESULT 1
AF272900
LOCUS
DEFINITION Homo sapiens core photoreceptor cyclic nucleotide-gated channel
beta subunit (CNGB3) mRNA, complete cds.
ACCESSION AF272900.1 GI:9247065
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 4369)
Kohl,S., Baumann,B., Broghammer,M., Jagle,H., Sieving,P.,
Keilner,U., Spegal,R., Anastasi,N., Zrenner,E., Sharpe,L.T. and

Pred. No. is the number of results predicted by chance to have a

Wissinger, B.
Mutations in the CNGB3 gene encoding the beta-subunit of the cone
photoreceptor cGMP-gated channel are responsible for achromatopsia
(ACHM3) linked to chromosome 8q21
Hum. Mol. Genet. 9 (14), 2107-2116 (2000)
20414632
PUBMED
10958649
2 (bases 1 to 4369)
Wissinger, B. and Kohl, S.
Direct Submission
Submitted (30-MAY-2000) University Eye Hospital, Molecular Genetics
Laboratory, Auf der Morgenstelle 15, Tuebingen D-72076, Germany
Location/Qualifiers
1. .4369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1. .4369
/gene="CNGB3"
47. .2476
/gene="CNGB3"
/codon_start=1
/product="cone photoreceptor cyclic nucleotide-gated
channel beta subunit"
/protein_id="AAF86274.1"
/db_xref="GI:9247066"
/translation="MFKSLTKVKNKPKIGENENBQSRNEEGSHPSNQSQTAAOE
ENKGEKSLKTKSTPTVSEPHNIDQKLSKNSGDLTNPDPQNAEPTGVPEBK
EMDPEKSPQKPPAPVINEYADQLNLVKNRQRTALYKKLAVGDSLSPBA
SPQAKTAPVPPKESDDKTEHYRLLWFKVKKMPTLEYLKRILKJNSIDSYDRLY
LLMLLVLTANMNCWFIPRLVFPYQADNIHWLADIIDIIYDMLFTQPRQLQ
FVRGDIITVDNELKRYRTSTKQLDVASIIPEDICYLPFGNPMFRANMLKYTEF
FEHNHLESIMDKAYIVIRITGVLFIHLINACVYMWASNEGIGTTRVWYDGEN
EYLCRYVAVATLTIGLPEPQTLFEIVFOLLNFFVGVFVSLICOMDRDVGAAFA
NONFRACMDTITAMNNYSIPKLVQKEVTVTWDSORMLDESLLAKTLPTTVOL
ALADIVNESIISKVDLPKCDTOMLYDMLRLKSLVLPDGFVCKKSEIKEMVYIKH
GEVVLGSPDGTQVLTILKAGSVFGBISLLAAGGNRRTANVAHGFAANLLTLDKKTLL
QEILVYFDSIRLKKARVLLKQKATAETAPRKDLALLFPPEKTPKPLKTLGG
TGKASRLALKKEQAAKKEEGEENEDKQKENEKQKENEKQKENEKQKENEK
DKGREPEKPLDRPECTASPIAVBEEPSHVARIVLPRGTSRQSLIISMAPSAGBEV
LTIEVKEKAKQ"

Query Match 100.0%; Score 2430; DB 9; Length 4369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTTAAATCGCTGACAAAAGTCAACAGGTGAAGCTATAGGAGAGAACAAATGAGAAT 60
DB 47 ATGTTTAAATCGCTGACAAAAGTCAACAGGTGAAGCTATAGGAGAGAACAAATGAGAAT 106
QY 61 GAAACAAAGTTCTGTCGAATGAAGAGGCTCTCACCCAAAGTAATCATGCTTCAGCAAAAC 120
DB 107 GAAACAAAGTTCTGTCGAATGAAGAGGCTCTCACCCAAAGTAATCATGCTTCAGCAAAAC 166
QY 121 ACAGCAGAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTC 180
DB 167 ACAGCAGAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTC 226
QY 181 ACCTCTGAAGGCCACACCAACATCAAGACAAACTCTCCAAGAAAAATTCCTCTGGA 240
DB 227 ACCTCTGAAGGCCACACCAACATCAAGACAAACTCTCCAAGAAAAATTCCTCTGGA 286
QY 241 GATCTGACCAACACCTGACCTCAAAATGACAGAGAACTGAGAGAGAGAGAGAGAGAGAG 300
DB 287 GATCTGACCAACACCTGACCTCAAAATGACAGAGAACTGAGAGAGAGAGAGAGAGAGAG 346
QY 301 CAGAAGGAAATGAGCCCGGAAAGAGAGGTCCAAACAGCCCAACAAACAAACCGCTGCA 360
DB 347 CAGAAGGAAATGAGCCCGGAAAGAGAGGTCCAAACAGCCCAACAAACAAACCGCTGCA 406
QY 361 GCTCCTGTATATAGTATGCGATGCCAGTCCAGCTACAAACCTGTGTAAGAAAGTGGCT 420
DB 1487 ACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAG 1546

Db 407 GTCCTCTTTATAAATGAGTATGCCGATGCCAGTACACAACTGGTGAAGAAATGCGT 466
QY 421 CAAAGAACACCCCTCTCAAGAAAAAGTTGGTAGAGGAGATCTCTCCTCACCCGAGCC 480
DB 467 CAAAGAACACCCCTCTCAAGAAAAAGTTGGTAGAGGAGATCTCTCCTCACCCGAGCC 526
QY 481 AGCCCAAACTCGAAAGCCCGAGGCTGTACACCACTGAAGAAAGAGGATGATAGCCA 540
DB 527 AGCCCAAACTCGAAAGCCCGAGGCTGTACACCACTGAAGAAAGAGGATGATAGCCA 586
QY 541 ACAGAACATTACTACAGGCTGTGTGGTTCAAAGTCAAAAGATGCTTTAAACAGAGTAC 600
DB 587 ACAGAACATTACTACAGGCTGTGTGGTTCAAAGTCAAAAGATGCTTTAAACAGAGTAC 646
QY 601 TTAAGCGAATTAACCTTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTG 660
DB 647 TTAAGCGAATTAACCTTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTG 706
QY 661 TGGCTCTTGGCTCACTCTTGCTATAACTGGAAGTCTGCTGTTTATACACCTGCGCTC 720
DB 707 TGGCTCTTGGCTCACTCTTGCTATAACTGGAAGTCTGCTGTTTATACACCTGCGCTC 766
QY 721 GTCTTCCCATATCAAAACCGCAGACCAACATACACTACTGCTTATTTGCGGACATCATGT 780
DB 767 GTCTTCCCATATCAAAACCGCAGACCAACATACACTACTGCTTATTTGCGGACATCATGT 826
QY 781 GATATCATCTACTCTTATGATATGCTTATTTATCCAGCCAGACTCCAGTTTGTAGAGA 840
DB 827 GATATCATCTACTCTTATGATATGCTTATTTATCCAGCCAGACTCCAGTTTGTAGAGA 886
QY 841 GGAGACATTAATAGTGGATTCAAATGAGCTAAAGAAACACTACAGGACTCTTACAAAATTT 900
DB 887 GGAGACATTAATAGTGGATTCAAATGAGCTAAAGAAACACTACAGGACTCTTACAAAATTT 946
QY 901 CAGTTGGATGTCGATCAATAATACATTTGATTTGCTACTCTCTTCTTGGGTTTAAAT 960
DB 947 CAGTTGGATGTCGATCAATAATACATTTGATTTGCTACTCTCTTCTTGGGTTTAAAT 1006
QY 961 CCAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCAC 1020
DB 1007 CCAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCAC 1066
QY 1021 CTAGAGTCTAATAGCAAAAGCATATATCTACAGAGTATTCGAACTGGATCTTG 1080
DB 1067 CTAGAGTCTAATAGCAAAAGCATATATCTACAGAGTATTCGAACTGGATCTTG 1126
QY 1081 CTGTTTATTTCTGCACATTAATGCCCTGTGTTTATTTACTGGCTTCAAACTATGAGGAAT 1140
DB 1127 CTGTTTATTTCTGCACATTAATGCCCTGTGTTTATTTACTGGCTTCAAACTATGAGGAAT 1186
QY 1141 GGCACCTACTAGATGGGTGTATGATGGGAAAGGAAACGAGTATCTGAGATGTTTATTTGG 1200
DB 1187 GGCACCTACTAGATGGGTGTATGATGGGAAAGGAAACGAGTATCTGAGATGTTTATTTGG 1246
QY 1201 GCAGTTCGAACCTTTAATTAACCAATGGTGGCTTCCAGAACCAACAACTTTTATTTGAAT 1260
DB 1247 GCAGTTCGAACCTTTAATTAACCAATGGTGGCTTCCAGAACCAACAACTTTTATTTGAAT 1306
QY 1261 GTTTTTCACCTCTTGAATTTTTTTTTCTGGAGTTTTTTTGTGTTCTCCAGTTTAAATTTGGT 1320
DB 1307 GTTTTTCACCTCTTGAATTTTTTTTTCTGGAGTTTTTTTGTGTTCTCCAGTTTAAATTTGGT 1366
QY 1321 ATGAGAGATGATGGAGAGCTACAGCCAAATGAGAACTACTTCCGCGCTCGATGAT 1380
DB 1367 ATGAGAGATGATGGAGAGCTACAGCCAAATGAGAACTACTTCCGCGCTCGATGAT 1426
QY 1381 GACACCATTCCTACATGAACAAATTAATCTCCATTTCTTAACTTGTGCAAAAGCGAGTTGG 1440
DB 1427 GACACCATTCCTACATGAACAAATTAATCTCCATTTCTTAACTTGTGCAAAAGCGAGTTGG 1486
QY 1441 ACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAG 1500
DB 1487 ACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAG 1546

ORIGIN

QY 1501 ACCCTACCACTACGGTCCAGTTAGCCCTCCGATTGATGTGAACCTTCAGCATCAACG 1560
 Db 1547 ACCCTACCACTACGGTCCAGTTAGCCCTCCGATTGATGTGAACCTTCAGCATCAACG 1606
 QY 1561 AAGTCCGCTTGTTCACAGGTTGTGATACACAGATGATTTATGACATGTTGCTAAAGATTG 1620
 Db 1607 AAGTCCGCTTGTTCACAGGTTGTGATACACAGATGATTTATGACATGTTGCTAAAGATTG 1666
 QY 1621 AATCCGCTTCTATTTCGCTGGTGACCTTCCTGCAAAAGGAGAAATGCGAAGGAA 1680
 Db 1667 AATCCGCTTCTATTTCGCTGGTGACCTTCCTGCAAAAGGAGAAATGCGAAGGAA 1726
 QY 1681 ATGTATATCATCAAGCATGGAAGTCCAAAGTCTTCTGGAGCCCTGATGGTACTTAAAGTT 1740
 Db 1727 ATGTATATCATCAAGCATGGAAGTCCAAAGTCTTCTGGAGCCCTGATGGTACTTAAAGTT 1786
 QY 1741 CTGGTACTTCGAAGCTGGTGGTGTGAGAAATCAGCTTCTAGCAGCAGAGGA 1800
 Db 1787 CTGGTACTTCGAAGCTGGTGGTGTGAGAAATCAGCTTCTAGCAGCAGAGGA 1846
 QY 1801 GGAACCCGTCGAATCCCAATGTGTGCGCCCAAGGTTTGCATCTTTAACTCTAGAC 1860
 Db 1847 GGAACCCGTCGAATCCCAATGTGTGCGCCCAAGGTTTGCATCTTTAACTCTAGAC 1906
 QY 1861 AAAAGACCTTCCCAAGAAATCTAGTGATTTATCCAGATTTGAAAGATCCTCATGAAG 1920
 Db 1907 AAAAGACCTTCCCAAGAAATCTAGTGATTTATCCAGATTTGAAAGATCCTCATGAAG 1966
 QY 1921 AAAGCCAGAGTGTCTTTAAAGCAGAGGCTAAGACCCGAGCAACCCCTCCAAAGAAA 1980
 Db 1967 AAAGCCAGAGTGTCTTTAAAGCAGAGGCTAAGACCCGAGCAACCCCTCCAAAGAAA 2026
 QY 1981 GATCTGGCTTCTTCCCAAGAGAGACACCCAAATCTTTAACTCTCTTA 2040
 Db 2027 GATCTGGCTTCTTCCCAAGAGAGACACCCAAATCTTTAACTCTCTTA 2086
 QY 2041 GGAGCCAGAGAAAGCAAGTCTTCAAGACTACTCAAAATGAAGCAGAGCAAGCAGCT 2100
 Db 2087 GGAGCCAGAGAAAGCAAGTCTTCAAGACTACTCAAAATGAAGCAGAGCAAGCAGCT 2146
 QY 2101 CAGAAGAAAGAAATCTGAAGAGGAGAGAGAGAAAGAAATGAAGTAAACAA 2160
 Db 2147 CAGAAGAAAGAAATCTGAAGAGGAGAGAGAGAAAGAAATGAAGTAAACAA 2206
 QY 2161 AAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAAGAAAGAAATGAAGATAA 2220
 Db 2207 AAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAAGAAAGAAATGAAGATAA 2266
 QY 2221 GATAAG 2280
 Db 2267 GATAAG 2326
 QY 2281 ATTGAGTGGAG 2340
 Db 2327 ATTGAGTGGAG 2386
 QY 2341 CGTCAATCACTATTATCAGATGGCTCTTCTGAGGCGGAGAGAGAGAGAGAGAGAGAG 2400
 Db 2387 CGTCAATCACTATTATCAGATGGCTCTTCTGAGGCGGAGAGAGAGAGAGAGAGAGAG 2446
 QY 2401 ATTGAAGTCAAGAAAG 2430
 Db 2447 ATTGAAGTCAAGAAAG 2476

RESULT 2
 AF228520
 LOCUS
 DEFINITION Homo sapiens cone photoreceptor cGMP-gated cation channel
 ACCESSION AF228520
 VERSION AF228520.1 GI:8843947

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2135)
 AUTHORS Sundin, O.H., Yang, J.M., Li, Y., Zhu, D., Hurd, J.N., Mitchell, T.N., Silva, E.D. and Maumenee, I.H.
 TITLE Genetic basis of total colourblindness among the Pingelapese islanders
 JOURNAL Nat. Genet. 25 (3), 289-293 (2000)
 MEDLINE 20347712
 PUBMED 10888875
 REFERENCE 2 (bases 1 to 2135)
 AUTHORS Sundin, O.H., Yang, J.-M., Li, Y., Zhu, D., Silva, E.D. and Maumenee, I.H.
 TITLE Direct Submission
 JOURNAL Submitted (23-JAN-2000) Ophthalmology, Johns Hopkins School of Medicine, 600 North Wolfe Street, Baltimore, MD 21287, USA
 FEATURES Location/Qualifiers
 source 1..2135

gene

CDS

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="8"
 /map="8q21-q22"
 /tissue_type="retina"
 1..2135
 /gene="CNGB3"
 244..2076
 /gene="CNGB3"
 /note="membrane channel; CNGA3; core channel domain"
 /codon_start=1
 /product="cone photoreceptor cGMP-gated cation channel beta-subunit"
 /protein_id="AAF80179.1"
 /db_xref="GI:8843948"
 /translation="MPLTEYLKRIKLPNSIDSYDRLYLWLVLVLTAYNNCCFPLRLNPEYQADNIHVLADIICDILVYDMLFIQPLQFVGGDIIVDSNELRKHVYRSTKQLDVASIIIPEDICILFFGNPMFRANRLKYTSFEPNHLISINDKAYIVRIKTYGLPILHINACVTYASNYEGITGRWYDGGNRYLCYTWAVRLLITIGLPIKQLVRFVQLLNFFSGVFVSLIGQMRDVIQAATNQNFVACMDITIAMNNYSIPKLVQRVFTWYETWDSORMLDESLLKLTPTVQLALADVNFIIISKVDLFGKDTOMIYDMLIRKSLVLYPGDFVCKEIGKENYIKHGEVQVLGPDGTGKVLVTLKAQSVLAAAGGNRRRTANVAHFANLTLDKLTQELVHYPSERILMKKARVLKQAKTAAEATPPKDLALLPPKPEETPKLTLLGGTGKASLARLLKLKREAQAKENSEGGEEGKENEKDKENEDKQENEDKQREPEKPLDRPECTASPIAVEE
 EPHSVRTVLPRGTSRSLISMAPAEAGGEEVLTVIEVKEKAKQ"

ORIGIN

Query Match 84.3%; Score 2049.4; DB 9; Length 2135;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 2075; Conservative 0; Mismatches 1; Indels 15; Gaps 1;
 QY 340 CCACAAACAAACCGCTCGAGCTCCTGTTATTAATGAGTATCCGATCCGATCCGAGCTACAC 399
 Db 1 CCACAAACAAACCGCTCGAGCTCCTGTTATTAATGAGTATCCGATCCGATCCGAGCTACAC 60
 QY 400 AACCTGGTGAAAGAAATGCGTCAAGAACAGCCCTCTTACAAAGAAAAGTTGGTAGAGGA 459
 Db 61 AACCTGGTGAAAGAAATGCGTCAAGAACAGCCCTCTTACAAAGAAAAGTTGGTAGAGGA 120
 QY 460 GATCTCTCTTACCGAGGAGCCCAACCTGCAAGCCCGAGCTGTGTACCAAGTAC 519
 Db 121 GATCTCTCTTACCGAGGAGCCCAACCTGCAAGCCCGAGCTGTGTACCAAGTAC 180
 QY 520 AAAGAAAGCGATGATAAGCCCAACAGAACATTACTACAGGCTGTGTGGTTTCAAGTCAAA 579
 Db 181 AAAGAAAGCGATGATAAGCCCAACAGAACATTACTACAGGCTGTGTGGTTTCAAGTCAAA 240
 QY 580 AAGATGCTTTAAGAGAGTACTTAAAGCGAATTAACCTTCAACAGCATAGATTATAC 639
 Db 241 AAGATGCTTTAAGAGAGTACTTAAAGCGAATTAACCTTCAACAGCATAGATTATAC 300

QY	640	ACAGATCGACTCTATCTCTCTGTGGCTCTTGCTTGTGCACCTCTTGCCCTATAAACCTGGAACTGC	699
DB	301	ACAGATCGACTCTATCTCTGTGGCTCTTGCTTGTGCACCTCTTGCCCTATAAACCTGGAACTGC	360
QY	700	TGTTTTATACCACTCGGCTCGTCTTCCCATATCAAAACCGCAGACAACATACACTACTCTGG	759
DB	361	TGTTTTATACCACTCGGCTCGTCTTCCCATATCAAAACCGCAGACAACATACACTACTCTGG	420
QY	760	CTTATTGGGACATCATATGTGATATCATCTACCTTTATGATGCTATGCTATTTATCCAGCC	819
DB	421	CTTATTGGGACATCATATGTGATATCATCTACCTTTATGATGCTATGCTATTTATCCAGCC	480
QY	820	AGACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACAC	879
DB	481	AGACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACAC	540
QY	880	TACAGGACTTCTACAAAATTTTCAGTTTGGATGTCGCACTCAATAATACCAATTTGATATTTGC	939
DB	541	TACAGGACTTCTACAAAATTTTCAGTTTGGATGTCGCACTCAATAATACCAATTTGATATTTGC	600
QY	940	TACCTCTCTTTGGGTTTAAATCCAAATGTTTAGAGCAAAATAGATGTTTAAAGTACACTTCA	999
DB	601	TACCTCTCTTTGGGTTTAAATCCAAATGTTTAGAGCAAAATAGATGTTTAAAGTACACTTCA	660
QY	1000	TTTTTTGAAATTAATCATCACTAGAGTCTATATATGGACAAGCAATATATCTACAGAGTT	1059
DB	661	TTTTTTGAAATTAATCATCACTAGAGTCTATATATGGACAAGCAATATATCTACAGAGTT	720
QY	1060	ATTCGAACTGATACCTGCTGTTTATCTCGACATTAATGCTGTGTTTATTTACTGG	1119
DB	721	ATTCGAACTGATACCTGCTGTTTATCTCGACATTAATGCTGTGTTTATTTACTGG	780
QY	1120	GCTTCAAATATGAAGGAATGGCACTACTAGATGGGTGATGGGAAGGAAACGAG	1179
DB	781	GCTTCAAATATGAAGGAATGGCACTACTAGATGGGTGATGGGAAGGAAACGAG	840
QY	1180	TATCTGAGATGTTATTAATGGGCAAGTTTTCGAACTTTTAATACCATGGTGGCTTCAGAA	1239
DB	841	TATCTGAGATGTTATTAATGGGCAAGTTTTCGAACTTTTAATACCATGGTGGCTTCAGAA	900
QY	1240	CCACAACTTTATTTGAAATGTTTTTCAACTCTGTGAATTTTTTTCTGGAGTTTTGTG	1299
DB	901	CCACAACTTTATTTGAAATGTTTTTCAACTCTGTGAATTTTTTTCTGGAGTTTTGTG	960
QY	1300	TTCTCCAGTTTAAATGGTCCAGATGAGAGTGTGATTCGACAGCTACAGCCAATCAGAC	1359
DB	961	TTCTCCAGTTTAAATGGTCCAGATGAGAGTGTGATTCGACAGCTACAGCCAATCAGAC	1020
QY	1360	TACTTCGCGCCCTGCATGGATGACACCAATTCGCTACATGAACAATTAATCCATTCCTAAA	1419
DB	1021	TACTTCGCGCCCTGCATGGATGACACCAATTCGCTACATGAACAATTAATCCATTCCTAAA	1080
QY	1420	CTTGTCGAAAGCGAGTTCCGACTGGTATGATATACATGGGACTCTCAAAGATGCTA	1479
DB	1081	CTTGTCGAAAGCGAGTTCCGACTGGTATGATATACATGGGACTCTCAAAGATGCTA	1140
QY	1480	GATGAGTCTGAATTTGCTTAAGACCCCTACCAACTACCGGTCCAGTTAGCCCTCGCCATTGAT	1539
DB	1141	GATGAGTCTGAATTTGCTTAAGACCCCTACCAACTACCGGTCCAGTTAGCCCTCGCCATTGAT	1200
QY	1540	GTGAATTCAGCATCATCAGCAAGTCGACTTGTTCAGGGTGTGATACACAGATGATT	1599
DB	1201	GTGAATTCAGCATCATCAGCAAGTCGACTTGTTCAGGGTGTGATACACAGATGATT	1260
QY	1600	TATGACATGTGCTAAGATTGAAATCCGTTCTCTATTTGCTGGTGGTACTTTGCTGCAAA	1659
DB	1261	TATGACATGTGCTAAGATTGAAATCCGTTCTCTATTTGCTGGTGGTACTTTGCTGCAAA	1320
QY	1660	AGGGGAAATTTGGCAAGAAATGATATCATCAAGCTGGAGAAGTCCAGTTCTTGA	1719
DB	1321	AGGGGAAATTTGGCAAGAAATGATATCATCAAGCTGGAGAAGTCCAGTTCTTGA	1380

QY	1720	GGCCCTGATGTAATAAGTCTCGGTTACTCTGAAAGCTGGTGGCGGTGTTTGAGAAATC	1779
Db	1381	GGCCCTGATGTAATAAGTCTCGGTTACTCTGAAAGCTGGTGGCGGTGTTTGAGAAATC	1427
QY	1780	AGCCTTCTAGCAGCAGGAGGAGAAACCGTGCACACTGCCAATGTGGTGGCCACGGGTTT	1839
Db	1428	--CCTTCTAGCAGCAGGAGGAGAAACCGTGCACACTGCCAATGTGGTGGCCACGGGTTT	1485
QY	1840	GCCAACTTTTAACTCTAGACAAAGACCCCTCCAGAAATTTCTAGTGCATTATCCAGAT	1899
Db	1486	GCCAACTTTTAACTCTAGACAAAGACCCCTCCAGAAATTTCTAGTGCATTATCCAGAT	1545
QY	1900	TCTGAAGGATCCTCATGAAGAAAGCAGAGTCTTTTAAAGCAGAAGGCTTAAGACCGCA	1959
Db	1546	TCTGAAGGATCCTCATGAAGAAAGCAGAGTCTTTTAAAGCAGAAGGCTTAAGACCGCA	1605
QY	1960	GAAGCAACCCCTCCAGAAAAAGATCTTTGCCCTCCTCTCCACCGAAAGAGACACCC	2019
Db	1606	GAAGCAACCCCTCCAGAAAAAGATCTTTGCCCTCCTCTCCACCGAAAGAGACACCC	1665
QY	2020	AAACTGTTTAAACTCTCTAGGAGGACACAGGAAAAAGCAAGTCTTCAAGACTACTCAA	2079
Db	1666	AAACTGTTTAAACTCTCTAGGAGGACACAGGAAAAAGCAAGTCTTCAAGACTACTCAA	1725
QY	2080	TTGAAGCGAGCAAGCAGCTCAGAGAAAGAAAAATTTGAGGAGGAGAGAGAAGCA	2139
Db	1726	TTGAAGCGAGCAAGCAGCTCAGAGAAAGAAAAATTTGAGGAGGAGAGAGAAGCA	1785
QY	2140	AAAGAAATGAAGATTAACAAAAAGAAAAATGAAGATTAACAAAAAGAAAAATGAAGATTA	2199
Db	1786	AAAGAAATGAAGATTAACAAAAAGAAAAATGAAGATTAACAAAAAGAAAAATGAAGATTA	1845
QY	2200	GGAAGAAATGAAGATTAAGATTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2259
Db	1846	GGAAGAAATGAAGATTAAGATTAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1905
QY	2260	CCTGAATGTACAGCAAGTCTTATTCAGTGGAGGAGAACCCCATCTCAGTTAGAAGGACA	2319
Db	1906	CCTGAATGTACAGCAAGTCTTATTCAGTGGAGGAGAACCCCATCTCAGTTAGAAGGACA	1965
QY	2320	GTTTTACCAGAGGAGTCTCTGTCATCATCTATTCAGATGGCTCTCTCTCTGAG	2379
Db	1966	GTTTTACCAGAGGAGTCTCTGTCATCATCTATTCAGATGGCTCTCTCTCTGAG	2025
QY	2380	GGCGGAGAGAGGTTCTTACTATTGAAGTCAAAAGAAAGGCTTAAGCAATAA	2430
Db	2026	GGCGGAGAGAGGTTCTTACTATTGAAGTCAAAAGAAAGGCTTAAGCAATAA	2076
RESULT 3			
AF490511			
LOCUS			
DEFINITION	AF490511	2826 bp mRNA linear	MAM 31-JUL-2002
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			

FEATURES		Hungerford Hill Rd., Ithaca, NY 14853, USA
source	1..2826	Location/Qualifiers
	/organism="Canis familiaris"	
	/mol_type="mrna"	
gene	/db_xref="taxon:9615"	
	1..2826	
	/gene="CNGB3"	
CDS	25..2373	
	/gene="CNGB3"	
	/codon_start=1	
	/product="cyclic nucleotide gated channel beta subunit"	
	/protein_id="AA089224.1"	
	/db_xref="GI:22023793"	
	/translation="MFKSLTIKSNKVKPRENDENKQDPDFSNQPPQSTROGENKSEN	
	KSLQNTKPTVTEESHAKMODKI SEKNLSRLDTTPNPHOHPTESKGAMSEQKEMBTGK	
	EGLVSPKSLPLGVPTVNEVADAGLNLVRMEQRTMLYKKLAEGBDISVYDRLVLLMOL	
	PLVAFSTQSNKLEKEHYHILCFKQKPLTEYLKSPFLPGSDISVYDRLVLLMOL	
	LVTIAYNMCHWLIPLRVFPYQPTDNTHFIIDICDIYLCDMLLLQPLQFLIKGG	
	DIMVDSNELKRYRSTKQLDVAIVMPDFVLPFGFNPFVRMRRLIKYTSFFFNH	
	HLESIMDKAYIRVIRITTCGLLYLTHINACIYVWASDYEGISTKRWYNGBNKYLR	
	YVWAVTLITIGLPEPQSFBIIVFOLLNFFSGVFVFSGLIQMDQDVTGAATANQNF	
	RISMVHTISYMTYSTPKNVONRVRTWYETWDSORMLDESLLCTLPVTMOLALTVD	
	VNLISLSVELPKGDQTMVDMLLKSTVYLPDGFVCKGEIGKEMVYIKOGSVQV	
	LGSDGQVIVILKAGAVGEISLLAGRGNRRTANVIAHGEPANLLTIDKLTOLIV	
	HYPDSEKLLMKASVLLKKAPATETTPPKGLAFLFPKQETPKI FRALLGGTQKAG	
	LTRLKLRQETQIKTSENSEEGGKRREYDKEREPSKILDSSECRANCIITASEMP	
	QSIRRAALPRGHTTRQSLIISMAPSABAGEVLITIEVKERAKQ"	
ORIGIN		
Query Match		69.2%; Score 1682.2; DB 4; Length 2826;
Best Local Similarity		83.6%; Pred. No. 3.4e-313; Indels 75; Gaps 3;
Matches 1972; Conservative		0; Mismatches 312;
QY	78	GAATGAAGAGGCTCTCACCAAGTAAATCAGTCTCAGCAAAACCAACAGCAGCAGGAGAGAAA 137
DB	84	GAATAACAAGATCCTGATCCAGCAATCAGCCTCAGCAATCTACAAGACAGGAGAGAAA 143
QY	138	CAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTCACGTCAGTGAAGAGCCACA 197
DB	144	CAAAAGTGAAGAAATCTCTCAAAACCAAGTCAATCCAGTCACGTCAGTGAAGAGAAATCA 203
QY	198	CACCAACATCAAGACAAATCTCCAAAGAAATCTCTCGAGATCTTGACCAACCAACCC 257
DB	204	TGCCAAATCGAAGATAATCTCCGAGAAATCTACTCAGAGACCTGACGACAAATCC 263
QY	258	TGACCTCAAAATGACAGCAACCACTGGAACTGCGCCAGAGAGAGAGAAATGAGACC 317
DB	264	CAACCATCAATCCAAAGAGATCAAAAGGGGCAATGTCAGAGCAGAGAGAAATGGAAC 323
QY	318	CGGGAAGAGAGGTCCAAACAGCCCAACAAACAAACCGCTGCGAGCTCTGTTAAATGA 377
DB	324	TGGGAAGAGAGGCTAGTCAGCCCAAAAGCAAAACCCCTTGGAGTCCCTGTTAAATGA 383
QY	378	GTATGCCGATGCCAGGTACACAACTTGTGAAAGAAATCGCTCAAGAAACAGCCCTCTA 437
DB	384	GTATGCTGATGCTCAGCTACACAACTTGTGAGAGGATCGCTCAAGAAACAAATGCTCTA 443
QY	438	CAAGAAAGAGTGTGAGAGGAGATCTCTCTCAACCCAGAGCCAGCCCAACAACTGCAA 497
DB	444	TAAGAAAGAGTGGCAGAGAGAGATATATCTCACTGAAAGCTAGCCCCCAACAACTGCAA 503
QY	498	GCCCAAGGCTTACCAACAGTAAAGAGAGAGATGATAAGCCAA---CAGAAACATTACTA 554
DB	504	GCCCAAGGCTTACCAACAGTAAAGAGAGAGATGATAAGCCAA---CAGAAACATTACTA 563
QY	555	CAGGCTGTGTGGTCAAAAGTCAAAAGATGCGCTTTAAACAGAGTACTTAAAGGAATTA 614
DB	564	TCACATATTGTGTTTAAATTCAGAGAGATGCGCTCTGACAGAGTACCTTAAACGATTA 623
QY	615	ACTTCCAAACAGCATAGATTCATACAGATGCGACTCTATCTCTGTGGCTCTGTGCTGT 674
DB	624	ACTTCCAGGAAGCATAGATTATACACAGATCGACTCTATCTCTGTGGCTCTGTGCTGT 683

QY	675	CACCTTTGCCCTATACTAGGAACCTGCTGGTTTATACCACTGGCGCTCGTCTTCCCATATCA 734
DB	684	CACCATTTGCCCTATACTAGGAACCTGCTGGTTTATACCACTAGCGCTCGTCTTCCCATATCA 743
QY	735	AAACCGCAGACAAATACACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCT 794
DB	744	AAACCGCAGACAAATACACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCT 803
QY	795	TTATGATATGCTATTTATCCAGCCCACTCCAGTTTGTAAAGAGGAGGAGACATAATAGT 854
DB	804	TTTGTATATGCTATTTATCCAGCCCACTCCAGTTTGTAAAGAGGAGGAGACATAATAGT 863
QY	855	GGATTCAATGAGCTAAGAAACACACACAGGCTTCTACAAAATTTTCAAGTTGATGTCGC 914
DB	864	GGATTCAATGAGCTAAGAAACACACACAGGCTTCTACAAAATTTTCAAGTTGATGTCGC 923
QY	915	ATCAATAATACCAATTTGATATTTTCTACCTCTCTCTTTGGGTTTAAATCCAATGTTAGAGC 974
DB	924	GTCAATAATGCAATTTGATATTTTCTACCTCTCTCTTTGGGTTTAAATCCAATGTTAGAGT 983
QY	975	AAATAGGATGTTAAAGTACACTTCAATTTTGAATTTTAAATCAACACCTAGAGTCTATAAT 1034
DB	984	GAATAGGATGTTAAAGTACACTTCAATTTTGAATTTTAAATCAACACCTAGAGTCTATAAT 1043
QY	1035	GGACAAAGCATATATCTACAGAGTATTTCGAAACAACTGGATACCTTGTGTTTATTCTGCA 1094
DB	1044	GGACAAAGCATATATCTACAGAGTATTTCGAAACAACTGGATACCTTGTGTTTATTCTGCA 1103
QY	1095	CATTAAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATG 1154
DB	1104	CATTAAATGCTGTGTTTATTACTGGGCTTCTGACTATGAAGGAATTTGGCACTACTAGATG 1163
QY	1155	GGTGTATGATGGGGAAGAAACGAGTATCTCAGATGTTATTATTGGGAGTTCGAACCTTT 1214
DB	1164	GGTGTATGATGGGGAAGAAACGAGTATCTCAGATGTTATTATTGGGAGTTCGAACCTTT 1223
QY	1215	AATTACCAATTTGGTGGCTTCCAGAACCAACAACTTTTCAAAATTTGTTTCAACTCTT 1274
DB	1224	AATTACCAATTTGGGAGCTTCCAGAACCAACAACTTTTCAAAATTTGTTTCAACTCTT 1283
QY	1275	GAATTTTCTTGGAGTTTGTGTTCTCCAGTTTAAATGCTCAGATGAGAGATGATGAT 1334
DB	1284	GAATTTTCTTGGAGTTTGTGTTCTCCAGTTTAAATGCTCAGATGAGAGATGATGAT 1343
QY	1335	TGGAGCAGCTACAGCAATCAGAACTACTTCCGCGCTTGCATGGATGATGATGATGATGAT 1394
DB	1344	TGGGAGCAGCTACAGCAATCAGAACTTCCGATCAGATGATGATGATGATGATGATGAT 1403
QY	1395	CATGAACAAATTAATCCATTTCTTAACTTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATA 1454
DB	1404	CATGAACAAATTAATCCATTTCTTAACTTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATA 1463
QY	1455	TACATGGGACTCTCAAGAAATGCTAGATGAGTCTCATTTGCTTAAAGCCCTACCAACTAC 1514
DB	1464	TACATGGGACTCTCAAGAAATGCTAGATGAGTCTCATTTGCTTAAAGCCCTACCAACTAC 1523
QY	1515	GGTCCAGTTAGCCCTCGCCATTTGATGTGAATTCAGATTCATCAGCAAAAGTGGATGTT 1574
DB	1524	CATGCAATTTAGCCCTCACTGTGGATGTGAATTCAGATTCATCAGCAAAAGTGGATGTT 1583
QY	1575	CAAGGTTGTGATACAGATGATTTATGACATGTTTGTGATGATGATGATGATGATGATGAT 1634
DB	1584	CAAGGTTGTGATACAGATGATTTATGACATGTTTGTGATGATGATGATGATGATGATGAT 1643
QY	1635	TTTGTCTGTGATGATTTGTCTGCAAAAGGAGGAGAAATTTGCAAGGAGAAATGATATCATCAA 1694
DB	1644	TTTGTCTGTGATGATTTGTCTGCAAAAGGAGGAGAAATTTGCAAGGAGAAATGATATCATCAA 1703
QY	1695	GAATGAGAGGTCGAAGTTCTTGGAGGCTCTGATGTTAAAGTCTTGGTACTCTGAA 1754
DB	1704	GCAAGGAGAGGTCGAAGTTCTTGGAGGCTCTGATGTTAAAGTCTTGGTACTCTGAA 1763

555 CAGGCTGTTGTTGTTCAAAAGTCAAAAGATGCTTTTACAGAGTACTTAAAGCGAATTAA 614
Db
617 CA---CGTTTTCTTTCAAAACCCAGAGAGTCCAGTAAAGAGACACCTACGAGAGTAATGAT 673
Qy
615 ACTTCCAAACAGCATAGATATCATACACAGATCGACTCTATCTCTGTTGGCTCTTCTCTTGT 674
Db
674 ACTTCCCAAGACATAGACTCTCTACACAGATCGGTCTATCTCTTGTGGCTCTCTCTTGT 733
Qy
675 CACTCTTGCTATTAAGTGAACCTGCTGTTTATACACCTGCGCTCGTCTTCCGATATCA 734
Db
734 CACCATTTGGGTATAACTGGAACCTTTGGCTGTACAGTGGCGCTCGTCTTCCGATGCA 793
Qy
735 AACCGCAGACACATACACTACTCTGCTTATTCGGACATCATATGTGATATCATCTACT 794
Db
794 AACACAGATACACAGAACTACTGATATTAAGTCTGATGATATCATCTACT 853
Qy
795 TTAAGATATGCTATTTATCAGCCAGACTCTCAGTTTGTAAAGAGGAGACATATAGT 854
Db
854 TTGTGATATACTATTGATCCAGCAAGACTCCCAATTTGTAAAGAGGAGGAGAAATATTGT 913
Qy
855 GGATTCAAATGAGCTAAGGAAACACTACAGGACTCTACAAATTTTCAGTTGGATGTGCG 914
Db
914 AGATTCAAATGAGCTGAGAGGAACTACCGAGTCTTACAAATTTTCAGTTGGATGTGCG 973
Qy
915 ATCAATTAATACCAATTTGATATTTGCTACTCTTCTTGGTATTAATTCATGTTAGAGC 974
Db
974 ATCTCTACTGCCATTCGAAAGTCTTACATCTCTTCTTGGAGTTTAAATCCAAATATTCAGAGC 1033
Qy
975 AAATAGAGTGTAAAGTACACTTCAATTTTGAATTTAATCATCATCTAGAGTCTATAT 1034
Db
1034 AAATCGGATATTAAGTATATCTTCTTGTAGTTTAAACATCATCTGGAGTCTATAT 1093
Qy
1035 GGCAAGAGCATATATACAGAGTATTCGAACAACTGGATCTTCTCTGTTTATTCGCA 1094
Db
1094 GGCACAAAGCATATGTCTACAGAGTCTCCGAACTCTGCTGTTTCTCCTGCA 1153
Qy
1095 CATTAATGCTGTTTATTTACTTGGGCTTCAAACTATGAAGAAATTTGGCACTACTAGATG 1154
Db
1154 CATTAAGCTGTTGTTTATTTACTTGGGCTTCAGACTATGAAGAAATTTGGCTAACTAAATG 1213
Qy
1155 GGTGTATGATGGGAGAGAAACAGATCTGAGATGTTATTTGGGCACTTCCAACTTT 1214
Db
1214 GGTCTATTAATGTTGAGGCAACAGATCTGCGATGCTTTATTTGGGCACTTCCAACTTT 1273
Qy
1215 AATTACCAATTTGGTGGCTTCCAGAACCAAACTTTATTTGAATTTGTTTTCACCTTT 1274
Db
1274 AATTACTATCGGGGCTTCCAGAGCCACAGACTTCATTTGAATTTGTTTTCACCTTT 1333
Qy
1275 GAATTTTTTCTGGAGTTTTTGTCTCCAGTTTAAATTTGTTGATGAGATGATGAT 1334
Db
1334 GAATTTTTTCTGGGCTTTTGTCTCCAGCTTAATTTGGTCAATGCGTGAATGAT 1393
Qy
1335 TGGAGCAGCTACAGCCCAATCAGAACTACTTCCGCGCTGATGATGATGACACCAATTCCTTA 1394
Db
1394 TGGGCGCAGCAACGCCAATCAGAACTACTTCCAGCGCTGATGATGATGATGATGAT 1453
Qy
1395 CATGAACAATTTACTCCATTTCTAACTTTGTGCAAAAGGAGTTCGGACTTGGTATGATA 1454
Db
1454 CATGAACAATTTACTCTATTTCTCAGAGTGTGCAATTCGAGTTTCGGACTTGGTTCGAATA 1513
Qy
1455 TACATGGGACTCTCAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATGATGAT 1514
Db
1514 TACATGGGACTCTCAAGAAATGCTAGATGATGATGATGATGATGATGATGATGATGATGAT 1573
Qy
1515 GGTCCAGTTAGCCCTCGCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1574
Db
1574 AATGAGTTGCTATTTGGCTTGCATATAAACTTCAGTATCATTCAGAAAGTGGAGTTATT 1633
Qy
1575 CAAGGTTGATACACAGATGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1634
Db
1634 CAAGGTTGATACACAGATGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1693
Qy
1635 TTTGCTGGTACTTTTGTCTCAAAAGGAGGAGAAATTTGGCAAGGAAATGTATATCATCA 1694

1694 TTTACCTGGTGACTTTTGTCTGCAAAAGGAGGAGAAATTTGCAAAAGAAATGTACATCATCAA 1753
Qy
1695 GCATGGAGAGTCCAAAGTCTTCTGGAGCCCTGATGATGATGATGATGATGATGATGATGATGAT 1754
Db
1754 ACAGGAGAGTCCAAAGTCTTCTGGAGCCCTGATGATGATGATGATGATGATGATGATGATGAT 1813
Qy
1755 AGCTGGGTCTGGTGTGTTGGAGAAATCAGCTTTCTAGCAGCAGGAGGAGGAAACCGTTCGAAC 1814
Db
1814 AGCTGGGTCTGGTGTGTTGGAGAAATCAGCTTTCTGGCAAAAGGAGGAGGAAATCGCCGAC 1873
Qy
1815 TGCCAAATGTTGGTGGCCCAAGGTTTCCAAATCTTTAACTCTAGACAAAAGACCTTCCA 1874
Db
1874 AGCTGATGTTTGGTGGCCCAAGGTTTCCAAATCTTTAACTCTAGACAAAAGACCTTCCA 1933
Qy
1875 AGAAATCTTCTGCTGATTTCCAGATTTCTGAAAGGATCTCTCATGAAGAAAGCAGAGTCT 1934
Db
1934 AGAAATCTTCTGCTGATTTCCAACTTTCTAAAGCTCTCTCATGAAGAAAGCAGAAATCT 1993
Qy
1935 TTTAAAGCAGAGGCTTAAGCCGAGAGCAACCCCTTCCAAAGAAAGATCTTGGCCTCT 1994
Db
1994 TTTAAAGCAGAGGCTTAAGCCGAGAGCAACCCCTTCCAAAGAAAGATCTTGGCCTCT 2053
Qy
1995 CTTCCCAAGGAGAGGAGCAACCCCAACTCTTTAACTCTCTAGAGGACACAGGAAA 2054
Db
2054 TTTCCCAAGGAGAGGAGCAACCCCAACTCTTTAACTCTCTAGAGGACACAGGAAA 2113
Qy
2055 AGCAAGTCTTCAAGACTACTCTAAATGAAAGCAGAGCAACCCCTTCCAAAGAAAGATCTT 2114
Db
2114 GGTGAGCTTTGGAGACTCTCTTAAAGGAAAGAGAAACCAACCTCAGAA----- 2164
Qy
2115 TTTCTAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2174
Db
2165 -----ATTAAGTGTAAAGTCTTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2195
Qy
2175 TAAACAAAAGAAATGAAGATAAAGGAAAGAAAGAAATGAAGATAAAGATAAAGGAGGAGGAG 2234
Db
2196 AAGAGGAAAGATATATGAAGACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2246
Qy
2235 GCCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2294
Db
2247 -----AAAAAACCACCTGGATAGTTCAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2301
Qy
2295 AGAACCCCACTCAGTTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2354
Db
2302 AATGTCCTCAATCAATTAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2361
Qy
2355 TATCAGCATGCTCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2414
Db
2362 CAGCAACATGG-TCTGCTACTGAGACTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2420
Qy
2415 AAAGGCTAAGCAATTA 2430
Db
2421 AAGGGCTAAGCAATTA 2436

RESULT 5
HUMNGCCB
LOCUS HUMNGCCB 3025 bp DNA linear PRI 01-MAY-1995
DEFINITION Homo sapiens clone hRCNC2a retinal rod cyclic nucleotide-gated cation channel gene, complete cds.
ACCESSION L15297
VERSION L15297.1 GI:291914
KEYWORDS cyclic nucleotide-gated cation channel; retinal protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3025)
AUTHORS Chen,T.Y., Peng,Y.W., Dhalluin,R.S., Ahamed,B., Reed,R.R. and Yau,K.W.
TITLE A new subunit of the cyclic nucleotide-gated cation channel in retinal rods

JOURNAL Nature 362 (6422), 764-767 (1993)
 MEDLINE 93226050
 PUBMED 7682292
 REFERENCE 2 (bases 1 to 3025)
 AUTHORS Ahamed, B.
 TITLE Direct Submission
 JOURNAL Submitted (17-MAY-1993) Basheer Ahamed, Biomedical Engineering,
 Johns Hopkins School of Medicine, Baltimore, MD 21205, USA
 COMMENT Original source text: Homo sapiens DNA.
 FEATURES Location/Qualifiers
 source
 1..3025
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="hRNC2a"
 /tissue_type="retinal"
 589..2460
 CDS
 /codon_start=1
 /product="cyclic nucleotide-gated cation channel"
 /protein_id="AA05619.1"
 /db_xref="GI:790520"
 /translation="MLCKFKHPKKYQPPQSIDPLTNLMYVLMFVVMANWNCW
 LIPVRAPPTQPNIRHLLMDYLDLITFDITVFQTLQFVRGDIITDKKMN
 NYLRRKFMLLSLLPDLFLYKGVNPLRLPRCLKYNWAFEFNRSLSIKAYV
 YRVITRAYLLSHLSCLYMASAYQGLSTHWYDVGVSFYRCYPAVRLTIT
 GGLPDKTLEIFVQLLNYFTGVPFASVIMQMRDVVGAATAGQTYRSCMDSTVKY
 NFYKIPKSVQRVNTVEYTHWSQMLDESELMVOLPKWRLDLADVNYISKVAL
 FQGGDROMI PMLKRLSVVLPNDYVCKGELGEMVYIIAGOVOLGSPDGKSLV
 TLXAGSVEGELSLLAVGGNRRTANVVAHGFNLFLDKDLNEILLVHYPESQKLK
 KARMLSNNKPKESKVLIPPRAGTTPKLFNALAMTGMKGKGAAGKLAHLRL
 KELAALBAAKHELVQAKSSQDVKGEGSAAPDQHPKBAATPPAPTPPPPG
 SPPSPPPASLGCEGEEGPAEPHESVIRICMSPGPEPGEILSVKMPBEREAK"

Query Match 23.8%; Score 577.4; DB 9; Length 3025;
 Best Local Similarity 64.3%; Pred. No. 6.1e-101;
 Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

QY 617 TTCAAACAGATAGATTACACAGATCGACTCTATCTCTGTGCTGCTTGTGTTGCA 676
 DB 635 TTCCCGAGAGATTGACCGGTGACCAACCTGATGATGCTATGCTTCTTCTGTTG 694
 QY 677 CTCTTGCTTAACTGGAATGCTGTTTATACACTGCGCTGCTTCCCATATCAA 736
 DB 695 TGAAGGCTGGAATTGGAATGTTGGCTGATTCCCGTGGCTGGGCTTCCCTACCA 754
 QY 737 CCGCAGACAAATACATCTACTGCTTATGGGACATCATATGATATCATCTACTTT 796
 DB 755 CCCCGACAAATACATCTACTGCTGCTGATGATGATGATGATGATGATGATG 814
 QY 797 ATGATATGCTTATTTATCCAGCCAGATCTCAGTTTGAAGAGAGAGACATATAGTG 856
 DB 815 TGGACATCACCGTGTTCAGACACGCTGCGATTTGTCAGAGGCGGGGACATCATAC 874
 QY 857 ATTCAAATGAGCTAAGAAACATCTACAGGACTTCTACAAATTTCAAGTTGCGAT 916
 DB 875 ACAAAGGACATCGGAAATAACTACTGAGTCTGCGCCCTCAAGATGGACCTGCTCA 934
 QY 917 CAATAATACATTTGATTTGCTTACTCTCTTTGGTTTAAATCCAAATTTTAGAGCAA 976
 DB 935 GCCTCTCGCTTGGATTTCTCTATTGAAAGTCGGTGTGAACCCCTCTCCGCTGC 994
 QY 977 ATAGATGTTAAAGTACATCTTATTTTGAATTTAATCATCATCTAGTGTATATGG 1036
 DB 995 CCGCTGTTTAAAGTACATGCTTCTCTAGTTTAAACAGCCGCTGGAATCATCTCA 1054
 QY 1037 ACAAGCATATATCTACAGAGTTATTTCGAACAACTGATCTGCTTTTATCTGCACA 1096
 DB 1055 GCAAAGCTACGTGTACAGGTCATCAGGACCAACAGCTTCTCTACAGCTGCAAT 1114
 QY 1097 TTAATGCTGCTGTTTATCTAGGCTTCAACTATGAGGAATTTGGCACTACTAGTGG 1156
 DB 1115 TGAATTCCTGCTTTATTTACTGGGATCGCCCTATCAGGCGCTTCCCTCACTACTGG 1174

QY 1157 TGTATGATGGGAAGAAACAGATATCTGAGATGTTATTATTGGCAGTTCGAACCTTAA 1216
 DB 1175 TTTACGATGGCGTGGAAACAGTATATTTCGCTGTACTTCTTGTGTGAAGACCTCA 1234
 QY 1217 TTACCAATTCGTCCTCCAGAACACAACTTTATTGAATTTCTTTCAACTTTGA 1276
 DB 1235 TACCAATCGGGGGCTGCTGACCCCAAGACACTCTTTGAAATTTCTTCAGAGCTG 1294
 QY 1277 ATTATTTTCTGGAGTTTCTCCAGTTTAAATTTGGTCAGATGAGAGATGATTTG 1336
 DB 1295 AATATTTTCAAGCGCTTTTCTCTGTGATGATCGGACAGATGAGAGATGTTG 1354
 QY 1337 GAGCAGTACAGCAATCAGAACTACTTCCGGCCCTGATGGATGACACCACTTGCCTACA 1396
 DB 1355 GGGCCGCCACCCGGGACAGACTTACCCGAGCTGATGACAGCAGCGTGAAGTACA 1414
 QY 1397 TGAACAAATTTACTCCATTCCTAACTTTGCAAAAGCAGTTTCGGACTTTGGTATGAATA 1456
 DB 1415 TGAATTTCTACAAGATCCCAAGTCGGTGCAGAACCCGCTCAAGACCTGTGTACAGTACA 1474
 QY 1457 CATGGACTCTCAAGAATGCTAGATGCTGTGATTTGCTTAAGACCTCACTCACTACGG 1516
 DB 1475 CCTGGCACTCGAAGCGATGCTGGATGATGATGATGATGATGATGATGATGATGATG 1534
 QY 1517 TCCAGTTAGCCCTCCCACTTGGATGAACTTCCAGCATCATCAGCAAACTGCACTTGTTC 1576
 DB 1535 TCGGCTGCACTCCCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1594
 QY 1577 AGGTTGTGATACACAGATGATTTATGATGATTTGCTTAAGATTTGAAATTCGTTCTT 1636
 DB 1595 AGGCTGTGTCGCGGAGATGATCTTTGATGATGATGATGATGATGATGATGATGATGAT 1654
 QY 1637 TCCCTGCTGCTTCTGTCGCAAAAGGAGAAATTTGGCAAGGAATGATATCATCAAGC 1696
 DB 1655 TCCCAACAGACTATGTCGCAAGAGAGGAGATGCGCCGTGAGATGATCATCATCAGG 1714
 QY 1697 ATGGAGAAGTCCAACTTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGAT 1756
 DB 1715 CAGGCAAGTGCAGCTCTTGGCGCCCTGATGATGATGATGATGATGATGATGATGATG 1774
 QY 1757 CTGGTCTGCTTTCGCAAAATCAGCTTCTAGCAGAGGAGGAGGAAACCGTGAACCTG 1816
 DB 1775 CTGGATCTGCTTTCGCAAAATGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1834
 QY 1817 CCAATGCTGGTGGCCACCGGTTTGGCAATCTTTAACTCTAGACAAAAGACCTCCAAG 1876
 DB 1835 CCAAGCTGTTGGCGACCGGTTTACCACTTCTTCATCTCTGATGATGATGATGATGAT 1894
 QY 1877 AAATCTAGTGCATTATCCAGATTCGAAAGATCTCATGATGAAAGAGCCAGAGTGTGTT 1936
 DB 1895 AGATTTGCTGCTTATCTGATGCTCAGAGTTTACTCCGGAAGAAAGCCAGGCGCATGC 1954
 QY 1937 TAAAGCAGAGGCTAAGACCGCAGAG 1963
 DB 1955 TGAGAGCAACAATAAGCCCAAGAGG 1981

RESULT 6
 HUMNGGCCA 3408 bp DNA linear PRI 01-MAY-1995
 LOCUS Homo sapiens clone hRNC2b retinal rod cyclic nucleotide-gated
 DEFINITION cation channel gene, complete cds.
 ACCESSION L15296
 VERSION L15296.1 GI:291913
 KEYWORDS cyclic nucleotide-gated cation channel; retinal protein.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3408)
 AUTHORS Chen, T.Y., Peng, Y.W., Dhallan, R.S., Ahamed, B., Reed, R.R. and
 Yau, K.W.

TITLE
 A new subunit of the cyclic nucleotide-gated cation channel in
 retinal rods
JOURNAL
 Nature 362 (6422), 764-767 (1993)
MEDLINE
 93226050
PUBMED
 7682292
REFERENCE
 2 (bases 1 to 3408)
AUTHORS
 Ahamed, B.
TITLE
 Direct Submission
JOURNAL
 Submitted (17-MAY-1993) Basheer Ahmed, Biomedical Engineering,
 Johns Hopkins School of Medicine, Baltimore, MD 21205, USA
COMMENT
 Original source text: Homo sapiens DNA.
FEATURES
 Location/Qualifiers
 1..3408
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="HRCNC2b"
 /tissue type="retinal"
 105..2834
 /codon_start=1
 /product="cyclic nucleotide-gated cation channel"
 /protein_id="AAA5620.1"
 /db_xref="GI:790511"
 /translation="MPRELSRIEKEEKEEEEEEEEEEEVEEVLDDSCVQVQVG
 VGSDEEGRSPQSTQDKLWEVEGEAKAEKAEAEVEAEAEAEKEPQWAEATK
 EPEAEAEASGPVATKQHPVEVEDTDADSCPLMAEENPPSTVLPSPAKSDTLI
 VSSASGTHRKLLPSDDAEELKALSPAESPVAWSKSDPTPKDQTDOPRAASTASTN
 SALINDKQLVLFKFERKKEKELIDPDVTSDESPKSPAKAPEAPATDKAEAA
 EPEVEHYDMLCKCKFKPKWKYQFQSIDPLNTLMYVLWLFVVMANWNCMLIPI
 RWAFYQPDNIHHMLMDYLCDLIYFLDITVFQTELRQVRGSDITDKKMNRYLK
 SRPKMDLISLLDDELYLVGVNPLLRPLCKLYMAFFENFSRLEILSKAYVVRV
 RTTAYLISHLNLSCLVYASVQGLGSHVYDVGNSVIRCYEYFAVKTLITIGLP
 DKPTLFEIYPLLNLVFTGFAPAFSMIGMEDVVGAATAGTQTVYRSCMDSTVKMNFYK
 IPKSNQRVKTWTEYIWHSGMDLSELMVQLPDKMLDLADIVNVIYVKVALFGCG
 DRMIEDMLKRSVYLPNDYVKGEGTGRENYIIQAGCVQLVQVGGPKSKSVLILKA
 GVSYETISLAVGGNRRNTANVAHGFTNLFLDKDLNELVHLYPESOKLRLKKAAR
 MLRSNNPKKEKSVLILPPRAGYPKLFNALAMTGMKGKAGKGLAHLRLKLELA
 ALPAAAKHEBLVQAKSDQVKEEGSAAPDQHTHPKEAATPPAPRTPEPPPPGPPS
 SPPPASLGSCEGEEGPAEPHEHSVLAICMSPGPEQILSVKMPBEREKAEE"
ORIGIN
 Query Match 23.8%; Score 577.4; DB 9; Length 3408;
 Best Local Similarity 64.3%; Pred. No. 6.1e-101;
 Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;
 QY 617 TTCCAAACAGCATAGATTTCATACACAGATCGACTTCCTCTGTGGCTCTTGGCTGTCA 676
 Db 1009 TTCCCCAGAGCATTGACCCGCTGACCAACTGATGATGTCCTATGCTGTTCTTCTGTGG 1068
 QY 677 CTCTTGTGCTATAACTGGAATCTGTGGTTTATACCACTCGCGCTCGTCTTCCCATATCAAA 736
 Db 1069 TGATGGCTGGAATTTGAACTGTGTGGCTGATTCCTGGTGGCTTCCCTTACCAGA 1128
 QY 737 CCGCAGACACATACATCTCTGGCTTATTCGGACATCATATGTGATATCATCTACCTTT 796
 Db 1129 CCCCGGACAACTCCACCACTGGCTGTGTGATGATACCTATCGGACCTCATCTACTTC 1188
 QY 797 ATGATATGCTATTTTATCCAGCCACAGATCCAGCTTTGTAAAGGAGGAGACATAATAGTGG 856
 Db 1189 TGGACATCACCGTGTTTCAGACACGCTGAGTTGTTCAGAGCGGGACATCATTTACGG 1248
 QY 857 ATTCAAATGAGCTAAGGAACACATACAGGACTTCTACAAATTTCACTTGGATGTGCGAT 916
 Db 1249 ACAAAGGACATCGAAATAACTACCTGAAGTCTCGCCGCTTCAGATGGAAGCTGTCTCA 1308
 QY 917 CAATAATACCATTTGATATTTGCTTACTCTCTTTTGGTTTATCCAAATGTTTAGACAA 976
 Db 1309 GCCTTCCTGCCCCTTGGATTTTCTCTATTGAAAGTCGGTGTGAACCCCTCTCTCGCCTGC 1368
 QY 977 ATAGATGTTTAAAGTACACTTCATTTTTCGAATTTAATCATCACTAGACTTATATGG 1036
 Db 1369 CCCGCTGTTTAAAGTACATGATGCCCTTCTTCGAGTTTAAACAGCGGCTTGGAAATCCATCTCA 1428

RESULT 7
HSU58837
LOCUS
DEFINITION
HUMAN CGMP-gated cation channel
beta subunit (CNCG2) mRNA, complete
cDNA
4033 bp
linear
PRI 18-JUL-1997
ACCSSION
U58837
VERSION
U58837.1
GI:1518638
KEYWORDS

RESULT 7
HSU58837
LOCUS
DEFINITION
HUMAN CGMP-gated cation channel
beta subunit (CNCG2) mRNA, complete
cDNA
4033 bp
linear
PRI 18-JUL-1997
ACCSSION
U58837
VERSION
U58837.1
GI:1518638
KEYWORDS

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     1 (bases 1 to 930)
            Ardell,M.D., Makhiya,A.K., Oliveira,L., Miniou,P.,
            Viegas-Pequignot,E. and Pittler,S.J.
TITLE       cDNA, gene structure, and chromosomal localization of human GAR1
            (CNGC31), a homologue of the third subunit of bovine photoreceptor
            cGMP-gated channel
JOURNAL     Genomics 28 (1), 32-38 (1995)
MEDLINE     96070429
PUBMED      7590744
REFERENCE   2 (bases 1 to 4033)
AUTHORS     Ardell,M.D., Aragon,I., Oliveira,L., Porche,G.E., Burke,E. and
            Pittler,S.J.
TITLE       The beta subunit of human rod photoreceptor cGMP-gated cation
            channel is generated from a complex transcription unit
JOURNAL     FEBS Lett. 389 (2), 213-218 (1996)
MEDLINE     96338110
PUBMED      8766832
REFERENCE   3 (bases 1 to 4033)
AUTHORS     Pittler,S.J.
TITLE       Direct Submission
            Submitted (20-MAY-1996) Pittler S. J., Department of Biochemistry
            and Molecular Biology, University of South Alabama College of
            Medicine, 307 University Blvd, Mobile, AL 36688-0002,USA
            Location/Qualifiers
FEATURES             1..4033
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="16"
                     /map="16q13"
                     /clone="hcc2"
                     /cell_type="rod photoreceptor"
                     /tissue_type="retina"
                     /dev_stage="adult"
                     1..4033
                     /gene="CNGC2"
                     1..57
                     /gene="CNGC2"
                     58..3813
                     /gene="CNGC2"
                     /function="modulation of channel activity"
                     /codon_start=1
                     /evidence=experimental
                     /product="cGMP-gated cation channel beta subunit"
                     /protein_id="AAB63387.1"
                     /db_xref="GI:1518639"
                     /translation="MLGVQRVLPPPGTFRKTMQEEVEPEPEAEVPEPEPNE
                     EAETESSMPPEESFKEEVEVAVADPSQPTKEAALTSTISLRAGQAEISEMNSPSHR
                     LTLMLGKVRVLPQVHSITEDPAQILHGSTGDTGCTDEPNEALRAQDTPGLRLLL
                     WLEQLRVLPPQPKSSEWRDEPAVATGAASDPAPGRQPMGPKLQARETSLPTP
                     IPLQPKKEEAPAEPEPGSQAOSSLPTRDPAPLVAWLHRLMALPQVPLHGKI
                     GEQPSGGLCDVQITSLPGQVPEPLVLEVEPEPEWEDAHQVSTPOGTEVPVAYE
                     EENKAVKMPRELRISEEDDEEEEEEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVE
                     DGTQPSTQSDQMEVEGEAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAEKAE
                     AEAASSVPATQHPQVEVDADSCPLMAEENPPSTVLPPSPAKSDTLVPSAS
                     GTRKRLPDEDEAEELKALSPAESPVVWSDPTTPKTDQDRAASTASTNSAIND
                     HQLVXLKFKERTKVKELIDPDVTSDESPKPSPAKAPAPAPDTKPAEAPVEE
                     RYCDMLCKFKRWKVKYQFQSDPLTNLMVYLFFVVMWNNWNLIPVRWAPPY
                     QTPNTHLLMDLDCILVFLDITVQFVGRGDIITDKKNNYLLKSRFKM
                     DLSSLPLDPLKLVGNVNLRLPRCLKNYAFEFNSRLSILSKAYVVRITAYL
                     LYSLHNSCLYHNASAQGLGSHVDVGNSTIRICYPFAVKILITIGLPPDKTLF
                     EIVFQLNLTGVFAFVMIGQMRVVGAAATAGOTYRSCMDVYKIMFYKIPKSVQ
                     NRKVTXYTWGSCMDSELMVQLPDRDLDAIDVNMIVSKVALFQGCQRMIF
                     DMLKRLSVYLVFNQYCKGEIGREMYIIQAGQVVLGPDGKSVLTKAGSVFGE
                     ISLIAVGGGNRRNTANVVAHGFTNLFILDKDLNEILVHVPESQKLKXKARMLRSNN
                     KPKEKSVLILPPRAGTPKLPNAALMTGKMGKGGKGLAHLRLKELALEAAA
                     KHLELVEQAKSSODVKEEGSAAPDOHTHPEATDPAPPTPEPGSPSPSPAS
                     LGSCEGEEGPAPPEEHSVLCMSPGPEFQELSVKMPFEEREKAE"
                     58..2851
misc_feature

```

QY	1397	TGAACAAATTACTCATTCCTAAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATATA	1456
Db	2768	TGAATTTCTAAAGATCCCAAGTCCGTGCAGAACCGGCTCAAGACTGGTACGAGTACA	2827
QY	1457	CATGGGACTCTCAAAAGATCTAGATGAGTCTGATTTGCTTAAAGACCCCTACCAACTACGG	1516
Db	2828	CCTGGCACTCGCAAGGATCTCGATGAGTGCAGAGCTGATGGTGCAGCTTCCAGACAAGA	2887
QY	1517	TCAGTTAGCCCTCGCCATGATGTGAACCTTACAGCATCATCAGCAAGTCGACTTCTTCA	1576
Db	2888	TGGGCTGGACCTCGCCATCGAGTGAACCTTACAGCATCGTTGCAAGTGGCTCTTCTT	2947
QY	1577	AGGCTTGTGATACACAGATGATTTATGACATGTTGCTTAAGATTGAAATCGTTCCTATT	1636
Db	2948	AGGCTGTGACCGCGCAGATGATCTTTGACATGCTGAAGAGCTTCGCTCTGTTGTCTACG	3007
QY	1637	TGCTGTGTGACTTGTCTGCAAAAGGAGAAATTCGCAAGGAAATGATATATCATCAAG	1696
Db	3008	TGCCCAACGACTATGTGTGCAAGAGGGGAGATCGGCCGTGAGATGTATCATCATCAG	3067
QY	1697	ATGAGAGAGTCCAAGTCTTTGGAGGCCCTGATGTAATAAGTTCGTGTTACTCTGAAAG	1756
Db	3068	CAGGCAAGTGCAGTCTTGGCGGCCCTGATGGGAAATCTGTGCTGGTACGCTGAAG	3127
QY	1757	CTGGCTCGGTGTTTGGAGAAATCAGCCCTTCTAGCAGCAGAGAGAAACCGTCGAACTG	1816
Db	3128	CTGGATCTGTGTTTGGAGAAATAAGCTTGTGCTGTGTTGGGGCGGGAACCGCGCACGG	3187
QY	1817	CCATGTGTGGTGGCCCGGCTTGCCTTCTTTAACTCTAGACAAAGACCCCTCCAAG	1876
Db	3188	CCACGTGGTGGCGCAGCGGTCTTACCAACCTCTTCATCTCGGATAGAGACTGAAATG	3247
QY	1877	AAATTTAGTGCATATCCAGATTCTGAAAGGATCTCTCATGAAAGACCGAGTGTCTTT	1936
Db	3248	AGATTTTGGTGCAITATCTCTGAGTCTCAGAAGTTACTTCGGAAGAACCGAGCGCATGC	3307
QY	1937	TAAAGCAGAGGCTAAGACCCGAGAAG	1963
Db	3308	TGAGAAGCAACAATAAGCCCAAGGAGG	3334
RESULT 8			
LOCUS	AF042498	4382 bp	mRNA linear PRI 02-MAR-1998
DEFINITION	Homo sapiens rod photoreceptor CNG-channel beta subunit (RCNC2)		
ACCESSION	AF042498		
VERSION	AF042498.1		
KEYWORDS	GI:2921582		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 4382)		
TITLE	Identification of a domain on the beta subunit of the rod		
JOURNAL	calcium-calmodulin		
REFERENCE	J. Biol. Chem. (1998) In press		
AUTHORS	2 (bases 1 to 4382)		
TITLE	Grunwald, M.E., Yu, W.P., Yu, H.H. and Yau, K.W.		
JOURNAL	Submitted (12-JAN-1998) Neuroscience, Johns Hopkins University		
FEATURES	School of Medicine, 725 N. Wolfe St., Baltimore, MD 21205, USA		
source	Location/Qualifiers		
gene	1..4382		
CDS	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	1..4382		
	/gene="RCNC2"		
	71..3808		
	/gene="RCNC2"		

/note="cyclic nucleotide-gated cation channel beta subunit"			
/codon_start=1			
/product="rod photoreceptor CNG-channel beta subunit"			
/protein_id="AAC04830.1"			
/db_xref="GI:2921582"			
/translation="MLGWQRVLPQPPGTPRKTKQEEVEPEPEMAEAVEPEPNPE			
EAETSESMPEEKEEVEAVADPQETKEAALTSTISLRQAQAEISEKNSPSHRV			
LTMKGVKEVTPQVHSITEDPAQILHGSTGDTGCTDEPNEALEAQDTPRQLLL			
WLEONLRLVPPPKSEVWRDPAVATPPGRPOEMGPKLQARETSLPTPIQLOPK			
BEPEAPAPEPQSGOATSLPTRPDLAVLHLEMLPQVLHGKIQEOEPD			
SPGCDVOTISILPGQVEPLVLEVEPPHEDAHQDVSTSPQTEVVPAAVEENKAV			
EKMPREJUREEKEEVEEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVEVE			
STSQKMEVEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEE			
GVPAKQHPVEQVEDTADSPVMAEENPPSTVLPSPAKSDTLIIPSSAGTHRKX			
LPSEDEAEELKALSPAESPVAADPTPKDTPDQDRAASTASTNSAIINDRIQELV			
CKFKERPKVKELIDPVTDSERPKSPKAPAPDTPKPAEAPVEBEHYCDML			
HHMLMDYLCILITFDLITVQTRQLQVRGGDIIDDKMNNYLKSRFRKMDLLSL			
PLDLYLVKGNPLRLRPLKYNWAFPEFNSRLESILSKATVYRVTATYLLSLHL			
NSCLYVASAYQGLSTHWYDGVNSYRCYFAVTLITIGGLPDPKTLFELFQL			
LNYETGVPAFVMIGQMDVDVGAATAGTYYRSCMDSTVKYNNFYKIPKSVONRVKTW			
YEYTWISQMDLDESLVQLPKVRLDLAIQVQVNLVSVKVALFOCQDRQMLFDMKRL			
RSVLYLNDYVCKGELGEMVYIIQAGOVVLGGPDGKSVLTLKAGSVFGEISLLAV			
GGRRRTANVAHGFTNLFILDKDLNELVHPESOKLRLKKRRMLRSNNKPKBEK			
SVLILPPRAGTPKLFNALAMTGMKGKAGKGLAHLRLRLKELAALEAAKQELV			
EOAKSQDVKGEGSAAPDQHTHPKBAATPPAPTPPEPPGSPSSPPPSLGRPEG			
BEFGPAEPEEHSVRICMSPGPEGEQLSVKXNPEEBEKA3"			
ORIGIN			
Query Match 23.8%; Score 577.4; DB 9; Length 4382;			
Best Local Similarity 64.3%; Freq. No. 5.9e-101; Indels 0; Gaps 0;			
Matches 866; Conservative 0; Mismatches 481;			
QY	617	TTCCAAAACAGCATAGATTATACACAGATCGACTCTATCTCTGTGGCTCTTGTGTCATCA	676
Db	1983	TTCCCCAGAGCATTCACCGCTGACCAACCTGATGTATGCTATGCTGCTTCTTCGTGG	2042
QY	677	CTCTTGGCTATAACTGGAACTGCTGTTTATACCACTGGCTCTCTTCCCATATCAA	736
Db	2043	TGATGGCTTGGAAATGGAACTGTTGGCTGATTCGGCTGGCTTCCCTACCCAGA	2102
QY	737	CGCGACAGACATACACTACTGCTTATTCGGGACATCATATGATATCATCTACCTTT	796
Db	2103	CCCCGACACATCCACCTGCTGCTGATGATTACCTATGCGACCTCATCTACTTCC	2162
QY	797	ATGATATGCTATTTATCCAGCCAGACTCCAGTGTGTAAGAGGAGAGACATAAGTGG	856
Db	2163	TGSACATCACCGTGTTCACAGACACGCTGCGAGTGTGTCAGAGCGGGGACATCATACGG	2222
QY	857	ATTCAAATGAGCTAAGGAAACACTACAGACTTCTACAAAATTCAGTTGGATGTCGCA	916
Db	2223	ACAAAAGGACATGCGAAATACCTACCTGAGTCTCGCGCTTCAAGATGGACCTGCTCA	2282
QY	917	CAATAATACCATTTGATATTTGCTACCTCTCTTTGGGTTTAAATCCATGTTTAGACAA	976
Db	2283	GCCTCTGCTGCTTGGATTTCTCTATTTGAAAGTCGGTGTGAACCCCTCTCCCGCTGC	2342
QY	977	ATAGGATGTAAGATACACTTCTATTTTGAATTAATCATCACCTAGAGTCTATAATGG	1036
Db	2343	COGCTGTTTAAAGATACATGGGCTTCTTCGAGTTTAAAGCGCGCTGGAATCACTCTCA	2402
QY	1037	ACAAAGCATATATCTACAGAGTTTATTCGAACAACTGGATACCTTGTGTTTATTTCGACA	1096
Db	2403	GCBAAGCTTACGTATACAGGTCATCAGGACCCACAGCTTACCTTCTACAGCTGCAAT	2462
QY	1097	TTAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGGATTTGGCATCTAGATGG	1156
Db	2463	TGAATTCCTGCTCTTTATTACTGGGCATCGGCTTATCAGGCGCTCGCTCCACTCTCTGGG	2522
QY	1157	TGTATGATGGGAAGGAAACGAGTATCTGAGATGTTTATTATTGGGAGTTCGAACCTTTAA	1216
Db	2523	TTTACGATGGCGTGGGAAACAGTTATTTCGCTGTCTACTACTTGTGCTGAAGACCTCA	2582

GGDIITDKXEMRNYYLKSRFFQDDLLCLLPDLFIYLYKLGJNPLRLPRCKYMAWFEF
NNRELELXKAVYVIRITAYLLYSHNSCLYFASAFQGTSHVVDYGVNGSY
RCYMAWKLITIGGLPQTPOTLFEVQLLNLYFVAFVSQIMQMDYVGAATAGT
VYFSCDSYTKVMYFPIPSRVQNVKRYWYEVHVSQMLDSESLWQDPKRWDLA
IDVNSYISXKVALFOGCDQOMFLDMLKRLSVLWYNDYTKCEIGREWYLYAQGV
QVUGSGDKAVLYTLKAGSVGEISLLAVGGNRRTANVAHGTFNLFLDKDLNEI
LVHYPSQULRKLKRAVRMNNKPKESQVLIILPPRAGTFPLAALAAAGKGPFG
AGKGLAHILRLKELAALAAARQOQLEKQASQAGEGSGATQDAPQPEPP
KDPKPPGPPPEPSAQSSPPPASAKPEESTGAPAPPPSVIRVSPGDFGEQTLVSVE
VLEKQEGEAF"

misc feature

920: .1489
VLEENKEGAE"

```
220. .1405  
/gene="Cnqb1"
```

```
/note="ion_tr
```

family contains Sodium, Potassium, Calcium ion channels. This family is 5 transmembrane helices in which the last two helices flank a loop which determines ion selectivity. In some sub-families (e.g. Na channels) the domain is repeated four times, whereas in others (e.g. K channels) the protein forms as a tetramer in the membrane. A bacterial structure of the protein is known for the last two helices but is not the pfam family due to it lacking the first four helices"

/db xref="CDD:pfam00520"
1784...2065

/db xref="CDD:pfam00520"

1784. .2065

/gene="Cngb1"

/note="cNMP_binding; Region: Cyclic nucleotide-binding

domain"

/db_xref="CDD:pfam00027"

ORIGIN

Query Match	23.7%	Score 575.2;	DB 10;	Length 4763;
Best Local Similarity	63.6%	Pred. No. 1.5e-100;		
Matches 915:	Conservative	0;	Mismatches 508;	Indels 15; Gaps 2;

617	QY	TTCCAAACAGCATAGATTCTATACACAGATCGACTCTATCTCCTCTGCGCTCTTGCTTGCA	676
783	Db	TC00CCAGAGTATCGACCCACTGACCAACCTCAATGATACATCTTTGGGCTGTTCTTTTGG	842
677	QY	CTCTTGCTATAACTCGAACTGCTGGTTTATACCACTGCGCTCGTCTTCCCATATAAA	736
843	Db	TGCTTGGCTTGGAACTGGAACTGCTGGCTGATCCCTGTGCGTGGGCCCTTCCGTACCAGC	902
737	QY	CCGAGACAACATACATCTACCTGCGTTATTTGGGACATCATATGATGATATCATCTACCTTT	796
903	Db	GGGCAGACAACATCCATCTTCTGGCTCCTCATGGATTACTTTGGCGACTTCATCTACCTCC	962
797	QY	ATGATATGCTATTTATCCAGCCACAGACTCCAGTTTGTAAAGAGGAGGACACATATAGTGG	856
963	Db	TGSACTATCACCGTGTTCAGATGCGCTTCAGTTGTCAAAGGCGGGACATCATTCAG	1022
857	QY	ATTCAAATGAGCTAAGGAACACATACAGACTTCTACAAAATTTTCAGTTGGATGTCGCAT	916
1023	Db	ACAAGAGGAGATCGGTATATAACTTACCTGAAGTCTGCGGTTTAAAGATGACCTGCTCT	1082
917	QY	CAATAATACCAATTTGATATTTGCTACCTCTCTTTGGGTTTAAATCCAAATGTTTACAGCA	976
1083	Db	GCCTTCCTCCCTTGGACTTCTCTACTTGAACCTGGCATCAACCCCTCTCCTTGCCTGC	1142
977	QY	ATAGAGTTTAAAGTACACTTCATTTTTTGAATTTAATCATCACTAGAGTCTATAATGG	1036
1143	Db	CCCCTGCCTGAAGTACATGCCCCTCTTTTGAGTTTATAACCGCCTGGAAGCATCTCTCA	1202
1037	QY	ACAAGCATATATCTACAGAGTTATTGCAACAACTGGGATCTTGCTGTTTATTTCTGCACA	1096
1203	Db	GCAAGCCCTACGTTTACAGAGTCAACAGCACAGGCCCTACCTGCTGTACAGCCTGCACC	1266
1097	QY	TTAATGCCCTGTTTATTACTGGGCTTCAAACTATGAAGGAATTTGGCATCTACTAGATGGG	1156
1263	Db	TCAACTCCTGCTTTTACTTGGGCATCAGCCCTCCAGGCACTCGGCTCCACTCACTGGG	1322
1157	QY	TGTATGATGGGAAGAAACGAGTATCTGAGATGTTATTTATTTGGGCAGTTTCCGACTTTAA	1216
1323	Db	TTTACGACGGAGTGGGGAACAGTTATATTCGATGCTACTTCTGGGCTGTGAAACCCCTCA	1386

AF074013	AF074013.1	GI:3309623	Bos taurus (cow)	857	ATTCAATAGAGCTAAGGAAACACTACAGGACTTCTACAAATTTTCAGTTGGATGTCGCAT	916
VERSION				1186	ACAAAAAGGAGATCGCAACAATTTACGTGAATCTCAGCGCTTTTAAATATGACATGCTCT	1245
KEYWORDS				917	CAATAATACCAATTTGATATTTGCTTACCTCTTTCTTTGGGTTTAAATCCAAATGTTTAGACAA	976
SOURCE				1246	GCCTCTTGGCCCTTGAGACTTACTTCTTAAATTCGGTGTGAATCCCTCTCTGGCTTGC	1305
ORGANISM				977	ATAGATGTTTAAAGTACACCTTCAATTTTGAATTTTATCATCACCCTAGAGCTCTAATAG	1036
REFERENCE				1306	CCCGCTGTTTGAAGTATATGGCTTCTTTGAGTTTAAACACCGCTGGAATCCATCTCA	1365
AUTHORS				1037	ACAAAGCATATATACAGAGTTTATCGAACCACTGGATCTTCTGTTTATTTCTGCACA	1096
TITLE				1366	GCAAGCCTTACGTTTACAGGTTTATCAGACACAGCTACTCTCTACAGCTTACATC	1425
JOURNAL				1097	TAAATGCTGTGTTTATTACTGGGCTTCAAACTAAGAAATTTGGCACTACTAGATGGG	1156
MEDLINE				1426	TGAATCATGCTCTTATTACTGGGCTATGGGCTATGGGCTCGGCTCCACTCAGTGGG	1485
PUBMED				1157	TGATATGTTGGGAAGAAACGAGTATCTGAGATGTTTATTTGGGCACTTCGAACTTAA	1216
REFERENCE				1486	TTTATGATGGGCTGGGAAACAGTTTACATTCGCTGTTACTCTGGGCTGTGAAGCCCTCA	1545
AUTHORS				1217	TTACCAATGTTGGCTTCCAGAACCAAACTTTTATTGAAATTTGTTTCAACTCTTGA	1276
TITLE				1546	TCACCATCGCGGCTGCGGCTATGGGCTATGGGCTCGGCTCCACTCAGTGGTCAA	1605
JOURNAL				1277	ATTTTCTTGGAGTTTGTGTTCTCCAGTTTAAATTTGTTGTTGTTGTTGTTGTTGTTG	1336
PUBMED				1606	ACTATTTTCAAGGCTGCTTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1665
REFERENCE				1337	GAGCAGCTACAGCAATCAGAACTACTTCCGCGCTCGATGGATGACACCACTTGCCTACA	1396
AUTHORS				1666	GGCGCCACACCGCGGACAGCTTACTACCGAGCTGATGACAGCAGCCGTTGAAGTATA	1725
TITLE				1397	TGAACAAATTTACTTCAATCTCTAACTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1456
JOURNAL				1726	TGAATTTCTTCAAGATCTCCAGTCTCGTGCAGAACCGGTTCAAGACCTGGTACGAATACA	1785
MEDLINE				1457	CATGGGACTCTCAAGAAATGCTAGATGATGTTGTTTGGTTTAAAGACCTTACCACCTAAGG	1516
PUBMED				1786	CTGGGACTCTCCAAAGCATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1845
REFERENCE				1517	TCCAGTTAGCCCTCGCAATTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1576
AUTHORS				1846	TGCGGCTGGAACCTGCGCAATTTGACGTGAACTATTTCATCGTCAGCAAGTGGCACTCTTCC	1905
TITLE				1577	AGGTTTGTGATACAGATGATTTATGATGTTTATGATGTTTATGATGTTTATGATGTTTATG	1636
JOURNAL				1906	AGGCTGTGACCGGCGAGATGATCTTTGATGATGTTGTTGTTGTTGTTGTTGTTGTTG	1965
MEDLINE				1637	TGCTGCTGCTGCTTGTCTCAAAAAGGGAGAAATTTGGCAAGGAAATGTATATCATCAAGC	1696
PUBMED				1966	TGCCCCAATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2025
REFERENCE				1697	ATCGAAGTCTCAAGTTCTTGGAGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1756
AUTHORS				2026	CGGGGAGGTGAGGTTCTTGGTGGGCTGAGTGGGAAATTCGGTCTGTTGTTGTTGTTG	2085
TITLE				1757	CTGGTCTGGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1816
JOURNAL				2086	CTGGAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2145
MEDLINE				1817	CCAATGTTGGTGGCCCGGTTTTCGAAATCTTTTAACTCTAGACAAAAGACCTCTCAAG	1876
PUBMED				2146	CTAACGTTGGTGGCCCGGTTTTCGAAATCTTTTAACTCTTTTCTTCTTCTTCTTCTTCT	2205
REFERENCE				1877	AAATTTAGTGCATTTTCCAGATTTCTGAAGGATCTCTCATGAAGAAGCCAGAGTGTCT	1936
AUTHORS				2206	AAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2265
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
PUBMED						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						

1919 AGGCTGTGACCGGAGATGATCTTTGACATGCTGAAGAGGCTGGCTGCTGTAGTCTACC 1978
 1637 TGCTGTGATCTTGTCTGCAAAAGGAGAAATGGCGAAGAAATGTATATCATCAGC 1696
 1979 TGCCCAATGATTAATGCTGCAAGAGGAGGAGATAGCCCGGAAATGTATATCATCAGC 2038
 1697 ATGAGAGAGTCCAAGTCTTGTGAGGCGCTGATGCTACTAAAGTTCCTGTTACTCTGAAG 1756
 2039 CGGGGAGGCTGAGGCTTGTGGTGGCCCGGATGGGAATCCGCTGCTGTGAGCTGAAG 2098
 1757 CTGGGTGGGTTTGGAGAAATCAGCCTTCTAGCAGAGAGAGAAACCGTGGAACTG 1816
 2099 CTGGATCTGTGTTCCGAGAAATAGCTTGTGCTGTAGGGCGGGAAACCGGCGACAG 2158
 1817 CCAATGTTGGGCGCCAGGTTTGCATCTTTTAACTCTAGACAAAAGACCTCCAAG 1876
 2159 CTAACGTTGGGCGCCATGGGTTTACCAACCTCTTCTTCTGATAGAGGACCTGAATG 2218
 1877 AAATTTCTAGTTCATATCCAGATTTCTGAAAGGATCTCTATGAAAGAGCAGAGTCTTT 1936
 2219 AAATTTCTGTTGATTTATCCCGAGTCTCAGAAGTTGCTCCGCAAGAGGCGGCGAATG 2278
 1937 TAAAGCAGAGGCTAGACCGCAGA 1961
 2279 TGAGAAATTAACAAGCCCAAGGA 2303

RESULT 13
 AF074014 3290 bp mRNA linear MAM 30-OCT-2001
 LOCUS Bos taurus cyclic nucleotide-gated channel beta subunit 1e
 DEFINITION (NCBbeta) mRNA, complete cds.
 ACCESSION AF074014
 VERSION AF074014.1 GI:3309625
 KEYWORDS Bos taurus (cow)
 SOURCE Bos taurus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 3290)
 Wiesner, B., Weiner, J., Middendorff, R., Hagen, V., Kaupp, U.B. and
 Weyand, I.
 Cyclic nucleotide-gated channels on the flagellum control Ca²⁺
 entry into sperm
 J. Cell Biol. 142 (2), 473-484 (1998)
 PUBMED 98345361
 9679145
 REFERENCE
 AUTHORS Wiesner, B., Weiner, J., Middendorff, R., Hagen, V., Kaupp, U.B. and
 Weyand, I.

TITLE Direct Submission
 JOURNAL Submitted (24-JUN-1998) IBI, PZ-Juelich, Leo-Brandt-Strasse,
 MEDLINE Juelich, NRW 52425, Germany
 PUBMED Location/Qualifiers
 REFERENCE
 AUTHORS 1. 3290
 2 (bases 1 to 3290)
 Wiesner, B., Weiner, J., Middendorff, R., Hagen, V., Kaupp, U.B. and
 Weyand, I.

FEATURES
 source
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 1. 3290
 /gene="CNCbeta"
 200..3058
 /gene="CNCbeta"
 /codon_start=1
 /product="cyclic nucleotide-gated channel beta subunit 1e"
 /protein_id="AAC26129.1"
 /db_xref="GI:3309626"

translation="MNVTAPLSSCTIMASLLAKTAPNHSVLLDSLYVPQSEEDRSSES
 ETQDSVEGGAQGEVGAQALSEESTQDSVEGGAQDOSEVGGGAQGEVGGAGAE
 QDVGGAQDQSTHQLQELAEALADSSGVPATEEHEPELQVEDADADSRPLTAENPPSP
 VOLPSPAKSTLAVFGATSGLSLRKRLPSQDDEAEELKMLSPASPVVMSDPTSPQ
 TDDQRTASQNSAIINDRLQELVKLFKRETKVKELIDPVTDSDESPKSPAK
 KAPEPAPEVKAFAQGEVEEHCYEMLOCKFKRKPWKYQFPQSIDPLTNLNLWLFF

ORIGIN
 Query Match 23.5%; Score 572.2; DB 4; Length 3290;
 Best Local Similarity 64.1%; Pred. No. 6.1e-100;
 Matches 862; Conservative 0; Mismatches 483; Indels 0; Gaps 0;
 617 TTCAAAACAGATGATTATACACAGATCGACTCTATCTCTCTGCTGCTTGTCTTGTCTG 676
 1146 TTCACAGAGATCGACCGCTGACCACTGATCTACATCTTGTGCTGCTTCTTCGTGG 1205
 677 CTCCTTGCCTATACTGGAACCTGCTGTTTATACCACTCGCGCTCGTCTTCCCATATCAA 736
 1206 TCGTGGCTTGGAACTGGAACCTGCTGCTGATTCCTCGTGGCTGGCCCTTCCCTATCAGA 1265
 737 CCGAGACAAATACACTACTGCTTATTCGCGGACATCATATGATATCATCTACCTTT 796
 1266 CGCCAGACAAATCACCTCTGCTGCTGATGATGATTAAGTACCTCATCTACCTCC 1325
 797 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGAGACATAATAGTGG 856
 1326 TGGACATCACCGTGTTCAGATGCGCTGCACTTGTTCAGAGGCGGGGACATCATTAAG 1385
 857 ATCAAAATGAGTAAGGAAACACTACAGACTCTTACAAAATTTTCAGTTGGATGCGCAT 916
 1386 ACAAAGAGAGATGCGCAAAATTAAGTAAATTCAGCGCTTAAAGATGGAATGCTCTCT 1445
 917 CAATAATACATTTGATATTTGCTTACCTCTTCTTGGGTTTAAATCAATGTTTAGAGCAA 976
 1446 GCCTCTTGGCTTGAATTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 1505
 977 ATAGGATGTAAGTACACTTCAATTTTGAATTTAAATCATCATCTAGAGTCTATAATGG 1036
 1506 CCGCTGTTTGAAGTATATGGCTTCTTCTTGAATTTAAACAAACCGCTGGAATCCATCTCA 1565
 1037 ACAGACATATCTACAGAGTATTCGAAACAACTGATACCTGCTGTTTATCTTCTGCACA 1096
 1566 GCAAGCCTACGTTTACAGGGTTTACAGACCAAGCTTACCTGCTCTACAGCTTACATC 1625
 1097 TTAATCGCTGCTGTTTATTAAGTCTTCAAACTATGAAGAAATGSCATCTAGATGG 1156
 1626 TGAATCATGCTCTTATTAAGTCTTCAAACTATGAAGAAATGSCATCTAGATGG 1685
 1157 TGTATGATGGGAGGAAACGAGATCTGAGATGTTTATTTATTTATTTATTTATTTATTT 1216
 1686 TTTATGATGGCGTGGGAAACAGTTACCTGCTGTTTACTTACTGCTGCTGCTGCTGCTGCT 1745
 1217 TTACCAATGCTGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTAACTCTTGA 1276
 1746 TCACCATCGCGGCTTCCCGACCCCGAGGCGCTCTTCTGAAATTTGCTTCCAGGCTTAA 1805
 1277 ATTTTCTTGGAGTTTGTGTTCTCCAGTTTAAATTTGATGATGAGATGATGATG 1336
 1806 ACTATTTCAGGGGCTTCTCGCTTCTCGGTCGATGATGATGATGATGATGATGATGATG 1865
 1337 GAGACCTACAGCAATCAGAACTTCTCGCGCTTCAATGATGATGATGATGATGATGATGATG 1396
 1866 GGGCGCCACCGGGGAGACAGCTTACTACCGAGCTGCAATGGACACACCGTGAAGTATA 1925
 1397 TGAACAAATTAATCTCCATTTCTTAAATTTCTTGTGAAAGCGAGTTCCGATCTGATATATA 1456
 1926 TGAATTTCTACAAGATCCCGAGGTCGCTGCGTGCAGAACCGGCTCAAGACCTGCTGATACATA 1985

Db 2577 GCCTTTGGCTTTGGATTTTCTCTACTTGAACCTTGGCGTGAACCCCTCTCTCGCCTGC 2636
QY 977 ATAGGATGTTAAGTACACTTCATTTTGTGATTTTAAATCANTCAGTAGAGTCTATATGG 1036
Db 2637 CCCGTGCGCTGAAGTACATGGCTTCTTTGAGTTTAAATACCGTCTGGAAGCCATCTCTCA 2696
QY 1037 ACAAGACATATATACAGAGTTATTCGAACAACTGGATACTTGTGTTTATTTCTGCACA 1096
Db 2697 GCANAGCTACGTTTACAGGTTATCAGACCAACCGCTACTCTGTATAGCTTGCATC 2756
QY 1097 TTAATGCCCTGTGTTTATTTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGGG 1156
Db 2757 TCAACTCTCTGCTTTTACTACTGGGCTGCGCTTCCAGGGCATCGGTTCCACTCACTGGG 2816
QY 1157 TGTATGATGGGAGAGAAACAGATATCTGAGATGTTATTTTGGGAGTTTCGAACTTTAA 1216
Db 2817 TTTATGACGGGTGGGGAACAGCTACATTCGATGCTACTCTGGGCTGTGAATACTCTCA 2876
QY 1217 TTACCAATTTGGGCTTCCAGAACCAAACTTTTATTTGAAATTTTCTTCAACTTTGA 1276
Db 2877 TCACCATCGAGGACTGCCGACCCAGACCGCTTTGAGATCGTCTCCAGCTGCTGA 2936
QY 1277 ATTTTCTTCTGGAGTTTCTGTTCTCCAGTTTAAATTTGTCAGATGAGAGATGTGATTG 1336
Db 2937 ATTATTTTACAGGTCTCTCGCTTTCTCTGTGATGTTGGACAGATGAGAGATGTGGTGG 2996
QY 1337 GAGCAGCTACAGCCAACTCAGAACTACTTCCGCGCTGCTGATGATGACACCATTTGCCCTACA 1396
Db 2997 GGGCGGCCACGGCGGAGACGCTACTACCGACCTGCATGGACAGCACCGGTGAGTACA 3056
QY 1397 TGAACAATTTACTCCATTTCTTAACTTTGTGCAAAAGCGAGTTCCGACTTGTATGAAATATA 1456
Db 3057 TGAACCTTCTACAGATCCCAAGTCTGTGCAGAACCGCGTCAAGACCTGGTACGAATACA 3116
QY 1457 CATGGGACTCTCAAGAAATGCTAGATGATGCTGATTTGCTTAAGACCTTACCACCTACGG 1516
Db 3117 CTTGGCACTCAAGGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3176
QY 1517 TCCAGTTAGCCCTCGCCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1576
Db 3177 TGCCTCTGGACCTGGCCATTGACGTAACTTCAACATTTGTCAAGAAAGTGGCGCTCTTCC 3236
QY 1577 AGGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTGAATCCGTTCTCTATT 1636
Db 3237 AGGGCTGGACCGGCAGATGATCTTCACATGCTCAAGCGACTTGGCTCAGTCTGCTACC 3296
QY 1637 TGCCTGTGACTTTGTCTGCAAAAGGGAGAAATTTGGCAAGGAAATGTATATCATCAAGC 1696
Db 3297 TACCCAATGACTATGTGTGCAAGAGGGGAGATTGGCCGAGAGATGTATATATCCAGG 3356
QY 1697 ATGAGAGATCCAAAGTTCTTGGAGGCCCTGATGGTACTAAAGTTCTGGTTACTCTGAAAG 1756
Db 3357 CGGGCGAGGTGCAAGGTCTGGGGGCCAGATGGAAGGCTGTCTTGGTGAACACTCAAG 3416
QY 1757 CTGGCTCGGTGTTTGGAGAAATCAGCCCTTCTAGCAGCAGGAGGAGAAACCGTCCGAATG 1816
Db 3417 CCGGATCGGTGTTTGGAGAGTAAGCTTCTGCTGTGGGGGGGTACAGGGCGACCG 3476
QY 1817 CCAATGTGGTGGCCCGCGGTTTGGCAATCTTTTAACTCTAGACAAAGAACCTTCCAAG 1876
Db 3477 CCAATGTGGTGGCCCGCGGTTTCAACAACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3536
QY 1877 AATTTCTAGTGCATTATCCAGATTTCTGAAGGATCTCTATGAAGAAAGCCAG 1928
Db 3537 AGATTTTGGTGCATTACCTTCAATCTCAGAACTGCTTCCGGAAGAGGCCAG 3588

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 18:18:50 ; Search time 6067.19 Seconds

(without alignments)
11960.251 Million cell updates/sec

Title: US-09-855-828-3

Perfect score: 2430

Sequence: 1 atgtttaatgcgtgacaaa.....aagaaagcctaagcaataa 2430

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_esti:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estcom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vri:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	815.8	33.6	2056	11 AK040140	AK040140 Mus muscu
2	553	22.8	553	10 BF725470	BF725470 Bx16c03.y
3	478	19.7	527	9 AL713036	AL713036 DKFZp686A
4	470	19.3	655	10 BB635459	BB635459 BB635459

C	5	430.2	17.7	437	10	BF725466
	6	402.4	16.0	1201	10	BE287002
	7	363.8	15.0	1201	13	BX401127
	8	320.8	13.2	468	9	AA069559
	9	308.4	12.7	978	13	BQ688992
	10	301.4	12.4	694	9	AU137778
	11	286.8	11.8	741	13	BX104558
	12	280.8	11.6	738	12	BI736222
C	13	280	11.5	423	12	BM938767
	14	279	11.5	445	14	H53423
	15	271.2	11.2	545	10	AW465556
	16	262.2	10.8	563	12	BG304577
C	17	261.6	10.8	503	9	AI150392
	18	234	9.6	247	9	AA317961
	19	232.4	9.6	270	9	AA012972
	20	224	9.2	325	10	BE982488
	21	219	9.0	696	13	BW269181
C	22	216.2	8.9	518	9	AV605886
	23	216.2	8.9	747	12	BI733974
	24	212.4	8.7	215	9	AA069498
	25	211	8.7	869	14	CD327412
	26	201.6	8.3	993	13	BX370500
	27	197.2	8.1	581	9	AV605887
	28	165.6	6.8	353	9	AL120448
	29	164	6.7	376	9	AL120239
C	30	162.2	6.7	674	29	CC498739
	31	137	5.6	832	12	BI827605
C	32	131.2	5.4	591	29	CC571022
	33	129.8	5.3	573	12	BM354832
C	34	120.6	5.0	535	9	AL928461
	35	111	4.6	920	13	BUI39545
	36	110.6	4.6	490	13	BQ639921
C	37	109.2	4.5	584	12	BM882371
	38	106.8	4.4	819	13	BU287884
	39	105.6	4.3	1215	28	CC245670
	40	102.8	4.2	795	13	BU291723
	41	97.6	4.0	573	29	CG985260
	42	96.6	4.0	706	9	AJ442203
C	43	94.4	3.9	800	29	CNS03HCK
	44	92.2	3.8	567	10	BF937274
C	45	91.4	3.8	712	13	BX416727

ALIGNMENTS

RESULT 1	AK040140	2056 bp	mRNA	linear	HTC 19-SEP-2003
LOCUS	AK040140	Mus musculus	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone: A3069G05	product:cyclic nucleotide gated channel beta 3, full insert sequence.	
DEFINITION	AK040140	AK040140.1	GI:26087649		
ACCESSION	AK040140	HTC; CAP trapper.			
VERSION	AK040140	Mus musculus (house mouse)			
KEYWORDS	AK040140	Mus musculus			
SOURCE	AK040140	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1	Carninci, P., and Hayashizaki, Y.			
AUTHORS	1	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	1	High-efficiency full-length cDNA cloning			
JOURNAL	1	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	1	99279253			
PUBMED	1	10349636			
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
AUTHORS	2	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
TITLE	2	Genome Res. 10 (10), 1617-1630 (2000)			
JOURNAL	2	20499374			
MEDLINE	2	11042159			
PUBMED	2				

REFERENCE AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, I., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861	Matches 1050; Conservative 0; Mismatches 252; Indels 53; Gaps 3; 1076 ACTTGTGTTTATTTCGCACATTAAATGCTGTGTTTATTACTGGGCTTCAACTATGAAG 1135 2 ACTTGTGTTTTCCTGCGCATTAAGCCTGTGTTTATTACTGGGCTTCCAGACTATGAAG 61 1136 GAATTGGCCTACTAGATGGGTGTATGATGGGGAAGAAACAGATATCTGAGATGTTATT 1195 62 GAATTGGCTCACTAAATGGTCTATAAAGGTGAAGGACAGATATCTGCGATGCTTTT 121 1196 ATTGGGCAGTTTGAACCTTTAAATACCATTTGGTGGCTTCCAGAACCAAACTTTATTG 1255 122 ATTGGGCAGTTTGAACCTTTAAATTAATTAATCGGGGGCTTCCAGAGCCAGACTTCAATTG 181 1256 AAATTGTTTTTCAACTCTTTGAATTTTTTTCTGGAGTTTTTCTGTTTCTCCAGTTTAAATG 1315 182 AAATTGTTTTTCAACTCTTTGAATTTTTTTCTGGGTTTTTCTGTTTCTCCAGCTTAAATG 241 1316 GTCCAGATGAGATGTGATTTGAGCAGCTTACAGCCAAATCAGAACTACTTCCGCGCTGCA 1375 242 GTCCAGATGCGTGTATGATTTGGGCGAGCAACAGCCAAATCAGAACTACTTCCAGCGCTGCA 301 1376 TGGATGACACCATTCCTCATGACAAATTAATCTCCATTCCTAACTTCTGCAAAAGCAG 1435 302 TGGACCATATCATTCCTCATGACAAATTAATCTTATTCCTCAGAGTGTGAGTATCGAG 361 1436 TTCCGACTTTGGTATGAATATATCATGGGACTCTCTCAAGAAATGCTAGATGAGTCTGATTTGC 1495 362 TTCCGACTTTGGTATGAATATATCATGGGACTCTCTCAAGAAATGCTAGATGAGTCTGATTTGC 421 1496 TTAAGACCTTACCACTACGTCAGTTCAGTTAGCCCTGCCATTCGATGATGAGTCTGAGTCA 1555 422 TTGAGAACCTTCCGAGCAGCAATGTCAGTTGTCTTATTTGCCCTTGACATAAATCTCAGTATCA 481 1556 TCAGCAAAAGTTCAGTTTTCAGGGTGTGATATACAGATGATTTATCAGATGTTGCTAA 1615 482 TCAGCAAGTGGAGTTTTCAGGGTGTGATATACAGGCTGTGACACAGATGTTTATGCTGTAA 541 1616 GATTGAATTCGTTTCTTATTTGCTGTGATCTTTGCTGCAAAAGGAGAAATTTGCA 1675 542 GATTGAATTCCTCACTATTTTATTTACCTGTGATCTTTGCTGCAAAAGGAGAAATTTGAA 601 1676 AGCAATGTATATCATCAAGCATGAGAAATGCAAGTTCTTTGGAGGCTCATGCTACTA 1735 602 AGCAATGTATCATCATCAACAGGAGTCCAGTCTTTGGAGGCTCATGCTGCTC 661 1736 AGTTTCTGTTTACTCTGAAAGTGGTGGTGTGTTGGAGAAATCAGCTTCTAGCAGAG 1795 662 AGTTTCTGTTTACTCTGAAAGTGGTGGTGTGTTGGAGAAATTAAGCTTCTGCAAAAG 721 1796 GAGGAGGAAACCGTCGAACTCCAGAAATTTCTAGTGCATTTATTCAGATTTCTCAAGGATCTCTCA 1915 782 TGGCAAAAGAGCTCTCCAGAAATTTCTGCTGCATTTATCCAACTTCTTAAAGCTCTCTCA 841 1916 TGNAGAAAGCCAGAGTGTCTTTTAAAGCAGAGGCTAGACCGGAGAGAACCCCTCCAA 1975 842 TGAAGAAAGCCAAATTTCTTTTAAAGCCAGAGGAGAAAGCCACTCAGGCAATCCCTGCAA 901 1976 GAAAGAGTCTTTCCTCTCTCTTCCACCGAAAGAGAGACCCCAAACTGTTTAAAACTC 2035 902 GACCAGGACCTGCTCTTCTTTTCCCAACCAAGAGAGAGACCCCGATGCTTAAAGTTC 961 2036 TCCTAGGAGGACAGAGAAAGCAAGTCTTTCAGAGTACTCAAAATTTGAAGCAGAGCAAG 2095 962 TCCTAGGAGGACAGAGAAAGTGGACCTTTGAGAGACTCTTTAAAGGAGAGAGAAACAA 1021 2096 CAGCTCAGAGAAAGAAATTTCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 2155 1022 CCACTCAGAA-----ATTAAGGTTGAAA 1043
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)	
REFERENCE AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2056) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission	
TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/.	
FEATURES	Location/Qualifiers source 1..2056 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:A430069G05" /db_xref="MGI:2404764" /db_xref="taxon:10090" /cnames="A430069G05" /tisue_type="thymus" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="0 day neonate" 1..2056 misc_feature /note="cyclic nucleotide gated channel beta 3 (MGI:1353562, GB NM_013927, evidence: BLASTN, 100%, match=2055)"	
ORIGIN	Query Match 33.6%; Score 815.8; DB 11; Length 2056; Best Local Similarity 77.5%; Pred. No. 2.2e-139;	

ORIGIN

2156 AACAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAAGAAAGAAATGAAG 2215
 Db 1044 GTTCCAAAGAAAGAAAGAAAGAAAGAAATGAAGATAAAGAAAGAAATGAAG 1103
 QY 2216 ATAAAGATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2275
 Db 1104 AAAAAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1149
 QY 2276 GTCCATATTCAGTGGAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2335
 Db 1150 GTTCTATACAGTGGAGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1209
 QY 2336 GTTCTCGTCAATCACTATACAGATGCTCTCTCTCTCTCTCTCTCTCTCTCT 2395
 Db 1210 ATGCTTATCAATGATCATCAGCAACATGG-TCCTGCTACTGAGCTGGAGAAGATTC 1268
 QY 2396 TTACTATTGAAGTCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2430
 Db 1269 TGACTATCAAGTCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1303

RESULT 2
 BF725470
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 553)
 Wistow, G.J., Bernstein, S., Behal, A. and Smith, D.
 NEBANK: EST analysis and bioinformatics for ocular genomics
 Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
 Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 16 row: C column: 03
 Seq primer: M13RPL reverse primer (ABI).
 Location/Qualifiers
 1. 553
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="bx16c03"
 /tissue_type="iris"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_lib="Human Iris cDNA (Un-normalized, unamplified): BX"
 Note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript plasmid system full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTTCTAGATCGGAGCGCGGCC(CT)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

FEATURES
 source

AL713036 527 bp mRNA linear EST 04-SEP-2003
 DKFZp686A1695_r1 686 (synonym: h1ccc3) Homo sapiens cDNA clone
 DKFZp686A1695_5', mRNA sequence.
 AL713036
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 527)
 Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and
 Wiemann, S.
 EST (Bioecker, H., Boecker, M., Brandt, P., Mewes, H.W., Weil, B. and
 Wiemann, S.)
 Unpublished (1999)
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GfB (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the

RESULT 3
 AL713036
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 527)
 Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and
 Wiemann, S.
 EST (Bioecker, H., Boecker, M., Brandt, P., Mewes, H.W., Weil, B. and
 Wiemann, S.)
 Unpublished (1999)
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GfB (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the

Query Match 22.8%; Score 553; DB 10; Length 553;
 Best Local Similarity 100.0%; Pred. No. 3.8e-91;
 Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1083 GTTTATTCTGCACATTAATGCCTGTGTTTATTACTTGGGCTTCAAACTATGAAGAAATGG 1142
 Db 1 GTTTATTCTGCACATTAATGCCTGTGTTTATTACTTGGGCTTCAAACTATGAAGAAATGG 60
 QY 1143 CACTACTAGATGGGTGATGATGGGAAAGAAAGAGATCTGAGATGTTATTATTGGGC 1202
 Db 61 CACTACTAGATGGGTGATGATGGGAAAGAAAGAGATCTGAGATGTTATTATTGGGC 120
 QY 1203 AGTTGCAACTTATTACCAATGGTGGCTTCCAGAACCAACAACCTTTATTGAAATGT 1262
 Db 121 AGTTGCAACTTATTACCAATGGTGGCTTCCAGAACCAACAACCTTTATTGAAATGT 180
 QY 1263 TTTTCAACTCTTGAATTTTTTTCTGGAGTTTTTGTCTTCCAGTTAAATTTGTCAGAT 1322
 Db 181 TTTTCAACTCTTGAATTTTTTTCTGGAGTTTTTGTCTTCCAGTTAAATTTGTCAGAT 240
 QY 1323 GAGAGATGTTGATTCGAGCAGCTACAGCAATCAGAACTACTTCCGCGCTGCATGGATGA 1382
 Db 241 GAGAGATGTTGATTCGAGCAGCTACAGCAATCAGAACTACTTCCGCGCTGCATGGATGA 300
 QY 1383 CACCAATGCCCTACATGAACAATTAATCTCCATTCCTTAACTTGTGCAAAAGCGAGTCGGAC 1442
 Db 301 CACCAATGCCCTACATGAACAATTAATCTCCATTCCTTAACTTGTGCAAAAGCGAGTCGGAC 360
 QY 1443 TTGTTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAGAC 1502
 Db 361 TTGTTATGAATATACATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAGAC 420
 QY 1503 CCTACCAACTAGGTCGCAAGTTAGCCCTGCGCAATGATGTAACCTCAGCATCATCAGCAA 1562
 Db 421 CCTACCAACTAGGTCGCAAGTTAGCCCTGCGCAATGATGTAACCTCAGCATCATCAGCAA 480
 QY 1563 AGTCGACTTGTTCAGAGGCTTGTGATACACAGATGATTATCACATGTTGCTTAAGATTGAA 1622
 Db 481 AGTCGACTTGTTCAGAGGCTTGTGATACACAGATGATTATCACATGTTGCTTAAGATTGAA 540
 QY 1623 ATCCGTTCTCTAT 1635
 Db 541 ATCCGTTCTCTAT 553

German Genome Project.

No sl sequence available.
This clone (DKFZp686A1695) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heuberweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

FEATURES

source
Location/Qualifiers
1..527
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686A1695"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 19.7%; Score 478; DB 9; Length 527;
Best Local Similarity 100.0%; Pred. No. 2e-77;
Matches 478; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTTTAATCGCTGACAAAAGTCAACAGGTGAAGCTATAGGAGAGAACAAATGAGAAT 60
DB 50 ATGTTTAATCGCTGACAAAAGTCAACAGGTGAAGCTATAGGAGAGAACAAATGAGAAT 109
QY 61 GAACAAAGTTCTGTCGGAATGAAGAGGCTCTCACCACCAAGTAATCACTCAGCAAAACC 120
DB 110 GAACAAAGTTCTGTCGGAATGAAGAGGCTCTCACCACCAAGTAATCACTCAGCAAAACC 169
QY 121 ACAGCACAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCACTCCAGTC 180
DB 170 ACAGCACAGGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCACTCCAGTC 229
QY 181 ACGTCTGAAGGCCACACCAACATACAGACAAATCTCTCAAGAAAAATTCCTCTGGA 240
DB 230 ACGTCTGAAGGCCACACCAACATACAGACAAATCTCTCAAGAAAAATTCCTCTGGA 289
QY 241 GATCTGACCAACACCTGACCTCAAAATGCAGCAGAACCACTGGAACAGTGCACAG 300
DB 290 GATCTGACCAACACCTGACCTCAAAATGCAGCAGAACCACTGGAACAGTGCACAG 349
QY 301 CAGAAGAAATGGACCCCGGAAAGAGGTCCTCAAAACAGCCACAAAACACCGCTGCA 360
DB 350 CAGAAGAAATGGACCCCGGAAAGAGGTCCTCAAAACAGCCACAAAACACCGCTGCA 409
QY 361 GCTCTCTTAAATAGTAGTATGCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCG 420
DB 410 GCTCTCTTAAATAGTAGTATGCGATGCCGATGCCGATGCCGATGCCGATGCCGATGCCG 469
QY 421 CAAGAAGACAGCCCTCTCAAGAAAAAGTTGGTAGAGGAGATCTCTCTCAACCCGAAG 478
DB 470 CAAGAAGACAGCCCTCTCAAGAAAAAGTTGGTAGAGGAGATCTCTCTCAACCCGAAG 527

RESULT 4
BB635459
LOCUS BB635459 RIKEN full-length enriched, 0 day neonate thymus Mus
DEFINITION musculus cDNA clone A43069G05 5', mRNA sequence.
ACCESSION BB635459
VERSION BB635459.1 GI:16471509
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 655)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

TITLE
JOURNAL
COMMENT

Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Waghi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES
source

Location/Qualifiers
1..655
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A43069G05"
/tissue_type="thymus"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate
thymus"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5', GAGAGAGATTCGAGTTAAATATTCCTCCCTCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

ORIGIN

Query Match 19.3%; Score 470; DB 10; Length 655;
Best Local Similarity 84.2%; Pred. No. 5.5e-76;
Matches 553; Conservative 0; Mismatches 101; Indels 3; Gaps 2;
QY 1078 TTGCTGTTTATCTGCACATTAATGCTGTTTATTACTGGCTTCAACTATGAGGA 1137

|||||
1 TTGCTGTTTCTCTGACATTAACCCCTGTGTTTATTACTGGGCTTCAGACTATGAAGA 60
1138 ATTGGCAGTCTAGATGGGTGATGATGGGGAAGAAACAGATATCTGAGATGTTATTAT 1197
|||||
61 ATTGGCTCACTAATGGGTCTATATGTTGAAGCAACAGTATCTGCGATGCTTTAT 120
1198 TGGCGAGTTGCAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1257
121 TGGCGAGTTGCAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 180
1258 ATTGTTTTCACTCTGTAATTTTTTTCTGGAGTTTGTGTTCTCCAGTTTAATTTGTT 1317
181 ATTGTTTTCACTCTGTAATTTTTTTCTGGAGTTTGTGTTCTCCAGTTTAATTTGTT 240
1318 CAGATGAGAGATGTTGATTCGAGCAGTACAGCAATCAGCAATCAGCAATCAGCAAT 1377
241 CAGATGCGTGTGATGTTGCGGCGAGCAACAGCAATCAGCAATCAGCAATCAGCAAT 300
1378 GATGACACCAATGCTTACATGACATTAATTAATTAATTAATTAATTAATTAATTAAT 1437
301 GACCATATCATTCCTTACATGACATTAATTAATTAATTAATTAATTAATTAATTAAT 360
1438 CGGACTTGTTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1497
361 CGGACTTGCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
1498 AGACGCTTACCACTAGTTCAGTTAGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1557
421 GAGAAGCTTCCGACAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 480
1558 AGCAAGTTCGACTTGTTCAGGCTTGTGATACACAGATGATTTATGACATGTTGCTTA 1617
481 GACAGTGGAGTATTCAGGCTGTGACACACAGATGATTTATGACCTGCTGCTAAGA 540
1618 TTGAATTCGCTTCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1677
541 TTGAATTCCTATTTATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
1678 GAATGATATCATCAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 1734
601 --AATGTACATCATCAA-CAGGAGAGTCCAAAGTCTCTGGAGGCTCTGATGCTACT 654

RESULT 5
BF725469/c 437 bp mRNA linear EST 05-JUN-2001
LOCUS
DEFINITION Bx16c03.x1 Human Iris cDNA (Un-normalized, unamplified): BX Homo
sapiens cDNA clone bx16c03 3', mRNA sequence.
ACCESSION
VERSION BF725469.1 GI:12041380
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 437)
Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
NETBANK: EST analysis and bioinformatics for ocular genomics
Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 16 row: c column: 03
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1. 437
/organism="Homo sapiens"
/mol_type="mRNA"

/db xref="taxon:9606"
/clone="bx16c03"
/tissue_type="Iris"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Iris cDNA (Un-normalized, unamplified):
BX"
/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORT6 vector
was constructed at Life Technologies, essentially
following the protocols of the Superscript Plasmid System
full details of which are contained in the manufacturer's
instruction manual (<http://www.lifetech.com/>). First
strand synthesis was carried out using a Not I
primer-adaptor
[5'-pGACTAGTTCCTAGATCGAGCGCGCC(T)15-3']. Not I/blunt
end inserts were cloned into the Not I/EcoR V sites in the
vector. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center (NISC)."
ORIGIN
Query Match 17.7%; Score 430.2; DB 10; Length 437;
Best Local Similarity 99.3%; Pred. No. 1.2e-68;
Matches 432; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1759 GGGTCGGTGGTGGAGAAATCAGGCTTCTAGCAGCAGGAGGAGGAAACCGTCGAACCTGCC 1818
Db 437 GGGTCGGTGGTGGAGAAATCAGGCTTCTAGCAGCAGGAGGAGGAAACCGTCGAACCTGCC 378
QY 1819 AATGTGTGGCCCGCGGTTTGGCAATCTTTTAACTCTAGACAAAGACCCCTCAAGAA 1878
Db 377 AATGTGTGGCCCGCGGTTTGGCAATCTTTTAACTCTAGACAAAGACCCCTCAAGAA 318
QY 1879 ATTCTAGTGCATTTATCCAGATTCCTGAAAGAGTCCCTCATGAGAAAGCCAGAGTGCTTTTA 1938
Db 317 ATTCTAGTGCATTTATCCAGATTCCTGAAAGAGTCCCTCATGAGAAAGCCAGAGTGCTTTTA 258
QY 1939 AAGCAGAAAGGCTTAAGACCGCAGAGCAACCCCTCCAGAAAGAGATCTTGGCCCTCTCTTC 1998
Db 257 AAGCAGAAAGGCTTAAGACCGCAGAGCAACCCCTCCAGAAAGAGATCTTGGCCCTCTCTTC 198
QY 1999 CCACGAAAGAGAGACACCCCACTGTTTAAACTCTCTAGGAGGACAGGAAAGCA 2058
Db 197 CCACGAAAGAGAGACACCCCACTGTTTAAACTCTCTAGGAGGACAGGAAAGCA 138
QY 2059 AGTCTTGAAGACTACTCAAAATTGAAGCGAGAGCAGAGCTCAGAGAAAGAAATTTCT 2118
Db 137 AGTCTTGAAGACTACTCAAAATTGAAGCGAGAGCAGAGCTCAGAGAAAGAAATTTCT 78
QY 2119 GAAGGAG 2178
Db 77 GAAGGAG 18
QY 2179 CAAAAG 2193
Db 17 CAAAAG 3
RESULT 6
BE287002
LOCUS
DEFINITION 601097229F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3496015 5',
trna sequence.
ACCESSION
VERSION BE287002
KEYWORDS
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 881)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-r@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLW8547 row: i column: 08
 High quality sequence stop: 774.
 Location/Qualifiers
 1..881
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:3496015"
 /tissue type="tumor, gross tissue"
 /dev stage="7 months"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Mam5"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

ORIGIN

Query Match 16.6%; Score 402.4; DB 10; Length 881;
 Best Local Similarity 73.9%; Pred. No. 1.2e-63;
 Matches 548; Conservative 0; Mismatches 171; Indels 23; Gaps 2;

QY 1459 TGGGACTCTCAAGAATCTAGATGAGTCTGATTGCTTAAGACCCCTACCACTAGGTC 1518
 Db 1 TGGAACTCACAAAGAACCTTAGATGATCCACTGCTTGAGAACCTCCCGACAGCATG 60

QY 1519 CAGTTAGCCCTCGCAATGATGTGAATCTCAGCATCATCAGCAAGTCGACTTGTTCAG 1578
 Db 61 CAGTTGTCTATTGCCCCCTGCATATAAATCTCAGTATCATCAGCAAGTGGAGTTATTCA 120

QY 1579 GGTGTGTATACAGATGATTTATGATGTTGCTAGATTTGAATCCGTTCTATTG 1638
 Db 121 GGCTGTGACACAGATGATTTATGACCTGCTGCTAAGATTGAATCCACTATTATTTA 180

QY 1639 CTTGGTCACTTTGTCTCAAAAAGGGAGAAATTTGGCAAGGAATGTATATCATCAAGCAT 1698
 Db 181 CCTGGTCACTTTGTCTCAAAAAGGGAGAAATTTGGAAAGAAATGTATCATCAACAC 240

QY 1699 GGAGAAGTCCAAAGTCTTGAGGCCCTGATGTTAAAGTCTTGTTACTCTGGAAGCT 1758
 Db 241 GGAGAAGTCCAAAGTCTTGAGGCCCTGATGTTGCTCAAGTCTGTTACTCTGGAAGCT 300

QY 1759 GGGTCGGTGTGTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTGAACCTGC 1818
 Db 301 G-----GCCCTTCTGCAAAAGGAGGAGGAATGCGCGACAGT 339

QY 1819 AATGTGTGGCCCGCCGCGTTTGCATTTTAACTCTAGACAAAAGACCCCTCCAGAA 1878
 Db 340 GATGTGTGGCCCGCCGCGATTGCGAATTTTAACTCTGACAAAAGACTCTCCAGAA 399

QY 1879 ATTCTAGTCAATATCCAGATTTCTGAAGGATCTCTCATGAAGAAACCGAGAGTCTTTTA 1938
 Db 400 ATTCTGTGATTTCAACTTCTTAAAGACTCTCTCATGAGAAACCGAATTCITTTA 459

QY 1939 AAGCAGAGCTTAAGCCCGCAGAGCAACCCCTCCAGAAAAGATCTTCGCCCTCTCTTC 1998
 Db 460 AGCCAGAAAGGGAAGACCACTCAGGCAATCCCTGCAAGACCAAGGACCTGCCCTCTCTTC 519

QY 1999 CCACCCAAAGAGAGACACCCCAAACTGTTTAAACTCTCTCTAGGAGGACAGGAAAGCA 2058
 Db 520 CCACCAAAAGAGAGACACCCCGAATGCTTAAAGTTCTCTTAGGACACACAGAGAGTGG 579

QY 2059 AGTCTTGCAGACTACTCAAAATTGAAGCGAGAGCAAGCAGCTCAG--AAGAAAGAAAT 2116
 Db 580 ACCTTGGAAAGACTCCTTAAGGAAAGAGAAAAAACAACCACTCAGAAATTAACCGTGAA 639

QY 2117 CTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2176
 Db 640 GTTCCACAGCGAAGAAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 699

QY 2177 AACAAAAGAAAATGAAGATA 2198
 Db 700 AGCAGAAAAGAGAAAATAA 721

RESULT 7
 EX401127
 LOCUS
 DEFINITION BX401127 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 cDNA clone CSODK009YE13 5-PRIME, mRNA sequence.
 ACCESSION BX401127
 VERSION BX401127.1 GI:30614460
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segret@genoscope.cns.fr; Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 7817.r For
 more information about this cluster, see
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODK009AC07QP1&cluster=7817.r>. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODK009AC07QP1.
 Location/Qualifiers
 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODK009YE13"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
 /cell_line="HELA"
 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
 source

ORIGIN

Query Match 15.0%; Score 363.8; DB 13; Length 1201;
 Best Local Similarity 60.8%; Pred. No. 1.2e-56;
 Matches 611; Conservative 35; Mismatches 353; Indels 6; Gaps 5;

QY 861 AAATGAGCTAGGAAACACACTCAGCACTCTACAAATTCAGTTGATCGCATCAAT 920
 Db 8 AAGGATATGCAATTAATCTACCTGAAAGTCTCGCGCTTCAAGATGACCTGTCAGCCT 67

QY 921 AATACCAATTTGATATTTGCTACCTCTTTCTTTGGGTTTAAATCCAAATGTTTGAAGCAATAG 980
 Db 68 CCTGCCCTTGGATTTCTCTATTGAAAGTCGGTGTGAACCCCTCTCTCGCGTGMCCG 127

QY 981 GATGTTAA--GTACACTTCATTTTGAATTTAATCATCACCTAGATGTATAATGGAC 1038

Db	128	CTGTTTAAATGATCATGCGCTTTCGAGTTTAAACAGCGCGCTGGAATCCATCTCTCAGC	187
Qy	1039	AAAGCATATATCTACAGAGTTATTCGAACAACCTGGATATCTGCTGTTTATTTCTGCACAT	1098
Db	188	AAAGCCTACGTGTACAGGCTCATCAGAYCAGAYTACCTCTTCTACAGCCTGCATTTG	247
Qy	1099	AATGCTGTGTTTATCTACCTGGCTTCAAACTATGAAGAAATGGCACTACTAGATGGGTG	1158
Db	248	AATTCCTGTCTTTTATCTACCTGGCTTCAAACTATGAAGAAATGGCACTACTAGATGGGTG	307
Qy	1159	TATGATGGGGAAGAAACAGATATCTGAGATGTTATTTATGGCAGTTCGAATTTAAT	1218
Db	308	TACATGCGCTGGGAAACAGATATATCTGCTGTTTCTGCTGTAACACCTCATC	367
Qy	1219	ACCATTTGGTGGCTTCCAGAACCAAACTTTATTTGAAATGTTTTCCTCACTCTTGAAT	1278
Db	368	AVCATCGGGGGCTGCTGACCCCAAGAVACTTTTGAATTTCTTCCAGCTGTGAAAT	427
Qy	1279	TTTTTTCTGGAGTTTCTGCTTCTCCAGTTTAAATGGTCAGATGAGATGTTGGA	1338
Db	428	TATTTACGCGGCTGCTTCTGCTGATGATTTGGCAGATGAGATGTTGTTAGG	487
Qy	1339	GCAGCTACAGCCCAATCAGAACTACTTCCGCGCTGCATGATGATGACACCATTCCTACATG	1398
Db	488	GCCGCCACCG-CAGACAGACCTACTACCGCAGCTGCATGACAGCAGCTGAAGTACATG	546
Qy	1399	AACATTTACTCCATCTTCTAACTTTGCAAAACGAGTTCCGACTTGGTATGATATATACA	1458
Db	547	AATTTTACAGATATCCCAAGTCCGTCAGAAACGAGTCAAGACCTGGTAAAGATGACCC	606
Qy	1459	TGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAGACCTCAACACTACGGTC	1518
Db	607	TGGCACTCGAAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG	666
Qy	1519	CAGTTAGCCCTCGCAATGATGAACTTCAGATCATCAGCAAGAAAGTGCATTTCAAG	1578
Db	667	CGGCTGACCTCGCATCGCATGATGATGATGATGATGATGATGATGATGATGATGATG	726
Qy	1579	GGTTGTGATACAGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATG	1638
Db	727	GGCTGTGACCGGAGATGATCTTTGATGATGATGATGATGATGATGATGATGATGATGATG	786
Qy	1639	CCTGGTGACTTTGCTGCAA-AAAGGAGAAATTTGGCAAGAAATGATATCATCAAGCA	1697
Db	787	CCCAACGACTATGTGTCAAGAAVGGSSAGATCGGCGCTGAGATGATCATCATCCAGGC	846
Qy	1698	TGGAGAGTCAAGTTCTTGGAGCCCTGATGATGATGATGATGATGATGATGATGATGATG	1757
Db	847	AGGCAAGTGCAGGCTTGGGCGSCCTGATGGAATCTGTCTGTGA-GCTKCAASY	905
Qy	1758	TGGCTGCTGTTTGGAGAAATCAGCTTCTAGCAGCAGGAGGAGAAACCGTCCAACTGC	1817
Db	906	KSSATYGTGTTTGSAGMAWAAGCTTGTGCTGTTTGGGGCGGCAA-DGGCGCAGGCC	964
Qy	1818	CAATGTGGTCCCAACGGTTTTCGAATCTTTTAACTCTTACAA 1862	
Db	965	CAAAAGTSGTGGSSWGGGTTTACVAMCTCTTATCTTATCTTATCTTATCTTATCTTATCT	1009
RESULT 8			
AA069559			
LOCUS			
DEFINITION			
zf75a04.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone			
IMAGE:382734 5', mRNA sequence.			
ACCESSION			
AA069559			
VERSION			
AA069559.1 GI:1576971			
KEYWORDS			
EST.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 468)			

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBue, T., Pavello, A., Gish, W., Hawkins, M., Hulman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, W., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Travaaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

97044478

8889549

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 874 Std Error: 0.00

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 382.

FEATURES

source

1...468

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:1290991"

/db_xref="taxon:9606"

/clone="IMAGE:382734"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares_pineal_gland_N3HPG"

/note="Organ: pineal gland; Vector: p7T3D (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTT
3', double-stranded cDNA was size selected, ligated to
Eco RI adapters (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified p7T3
vector (Pharmacia). Library constructed by Bento Soares
and M.Fatima Bonaldo."

ORIGIN

Query Match 13.2%; Score 320.8; DB 9; Length 468;

Best Local Similarity 97.9%; Pred. No. 1.2e-48;

Matches 325; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 19 AAAGTCAACAAGGTGAAGCCTATAGGAGAGAACATGAGAAATGAACAAAGTTCTCGTCGG 78

Db 2 AAAGTCAACAAGGTGAAGCCTATAGGAGAGAACATGAGAAATGAACAAAGTTCTCGTCGG 61

Qy 79 AATGAAGAAGGCTCTCACCAGTAATCAGTCTCAGCAACCCACAGCAGCAGGAAGAAAC 138

Db 62 AATGAAGAAGGCTCTCACCAGTAATCAGTCTCAGCAACCCACAGCAGCAGGAAGAAAC 121

Qy 139 AAAGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTCCAGTCTGAGAGCCACAC 198

Db 122 AAAGTGAAGAGAAATCTCTCAAAACCAAGTCAATCCAGTCCAGTCTGAGAGCCACAC 181

Qy 199 ACCAATACAGACAAACTCTCCAAAGAAAATTCCTCTGGAGATCTGACCAACACCT 258

Db 182 ACCAATACAGACAAACTCTCCAAAGAAAATTCCTCTGGAGATCTGACCAACACCT 241

Qy 259 GACCTCAAAATGCAGCAGAACCACTGAAACAGTGCAGAGCAGAGAAATGACCC 318

Db 242 GACCTCAAAATGCAGCAGAACCACTGAAACAGTGCAGAGCAGAGAAATGACCC 301

Qy 319 GGAAGAAGAGGTCCAAACAGCCCAACAAACAA 350

Db 302 GGAAGAAGAGGTCCAAACAGGTGACCCCTAGAA 333

RESULT 9

BQ068992

```

LOCUS      BQ068992              978 bp      mRNA      linear      EST 02-APR-2002
DEFINITION AGENCOURT_6740166 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802872
            5', mRNA sequence.
ACCESSION  BQ068992
VERSION    BQ068992.1 GI:19898038
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 978)
            NIH-MGC http://mgi.nci.nih.gov/
AUTHORS    National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
COMMENT    Email: cgabs-remail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCW2037 row: p column: 09
            High quality sequence stop: 726.

FEATURES             source
     source
     1..978
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="IMAGE:5802872"
         /tissue_type="neuroblastoma, cell line"
         /lab_host="DH10B (phage-resistant)"
         /clone_lib="NIH_MGC_47"
         /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
         EcoRI; cDNA made by oligo-dT priming. Directionally
         cloned into EcoRI/XhoI sites using the following 5'
         adaptor: GCACGAG(G). Size-selected >500bp for average
         insert size 1.8kb. Library constructed by Ling Hong in
         the laboratory of Gerald M. Rubin (University of
         California, Berkeley) using ZAP-cDNA synthesis kit
         (Stratagene) and Superscript II RT (Life Technologies).
         Note: this is a NIH_MGC Library."

ORIGIN
Query Match      12.7%; Score 308.4; DB 13; Length 978;
Best Local Similarity 67.7%; Pred. No. 1.8e-46;
Matches 432; Conservative 0; Mismatches 206; Indels 0; Gaps 0;

Qy 1326 AGATGTGATTGGAGCAGTACAGCAATCAGCACTTCCGGCGCTGCATGGATGACAC 1385
Db 1 AGATGTGTAGGGCCGCCCGGGGACAGACCTACTACCGAGCTGCATGGACGAC 60

Qy 1386 CATTCGCTACATGAACAATTACTCCATCTCTAACTTGTCGAAAGGAGTTCGGACTTG 1445
Db 61 GGTGAAGTACATGAATTTCTACAGATATCCCAAGTCGCTGCAGAACCGGTCAAGACCTG 120

Qy 1446 GTATGAATATACATGGGAGCTCTCAAGAATGCTAGATGAGTCTGATTGCTTAAGACCT 1505
Db 121 GTACGAGTACACCTGGCACTCGGAGGCGATGCTGATGAGTCAAGCTGATGTCGAGCT 180

Qy 1506 ACCAACTACGGTCCAGTAGCCCTTCGCCATGATGAACTTCAGCATCATCAGCAAGT 1565
Db 181 TCCAGACAAGATGGCGTGGACCTCGCATCGAGCTGAACATCAACATCGTTAGCAAGT 240

Qy 1566 CGACTTCTTCAAGGGTGTGATACACAGATGATTATGACATGCTGCTAAGATTGAATC 1625
Db 241 CGACTCTTTCAGGGCTGTGACCGGAGATGATCTTGACATGCTGAAGAGGCTTCGCTC 300

Qy 1626 CGTTCCTATTTCCTGGTGACTTTGTCGCAAAAAGGGGAAATTTGGCAAGAAATGTA 1685
Db 301 TGTGTCTACTGTCCTCCCAACGACTATGTGTGCAAGAGGGGGAGATCGGCCGTGAGATGTA 360

```

```

Qy 1686 TATCATCAAGCATGAGAAATCCAAAGTCTTCTGAGGCCCTGATGGTACTAAAGTTCTGGT 1745
Db 361 CATCATCCAGGAGGCGAGTGCAGGCTCTTGGCGGCCCTGATGGAAATCTGTGCTGT 420

Qy 1746 TACTCTGAAAGCTGGGTGCTGTTGGAGAAATCAGCCTTCTAGCAGAGGAGGAGAAA 1805
Db 421 GACGCTGAAAGCTGGATCTGTGTTGGAGAAATAGCTTGTGCTGTTGGGGGGGAA 480

Qy 1806 CCGTCGAACTGCCAAATGCTGSCGCCACGGGTTTCCCAATCTTTAACTCTAGACAAA 1865
Db 481 CCGCGCAGCGCCACGCTGTGGCGACGGGTTTACCAACCTCTTCATCCTCGATAAGAA 540

Qy 1866 GACCTCCAGAAATTTCTAGTCATTCAGATTTCTGAAGATCTTCAAGAAAGC 1925
Db 541 GGACCTGAATGAGATTTTGGTGCATTCCTGAGTCTCAGAGTTACTCCGGAAGAAAGC 600

Qy 1926 CAGAGTGTCTTTAAGCAGAGGCTAAGACCCAGAG 1963
Db 601 CAGGCGCATGCTGAGAAAGCAACAATAGCCCAAGGAGG 638

RESULT 10
LOCUS     AU137778              694 bp      mRNA      linear      EST 02-AUG-2002
DEFINITION AU137778 PLACE1 Homo sapiens cDNA clone PLACE1007225 5', mRNA
            sequence.
ACCESSION  AU137778
VERSION    AU137778.1 GI:10999299
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 694)
AUTHORS    Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
TITLE      HRI human cDNA project
JOURNAL    Unpublished (2000)
COMMENT    Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
            Research Institute; cDNA library construction; Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.

FEATURES             source
     source
     1..694
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="PLACE1007225"
         /tissue_type="placenta"
         /clone_lib="PLAC1"
         /note="Vector: pME18SFL3"

ORIGIN
Query Match      12.4%; Score 301.4; DB 9; Length 694;
Best Local Similarity 66.3%; Pred. No. 3.8e-45;
Matches 445; Conservative 0; Mismatches 225; Indels 1; Gaps 1;

Qy 1049 TCTACAGAGTTATTCGACAACTGATGATGCTGTTTATTTCTCCATTAATCCCTGTG 1108
Db 20 TCTGAGGGTTCATCAGGACCAAGCCCTTCTCTACAGCCTCATTTGAATTCCTGTC 79

Qy 1109 TTTATTACTGGGCTTCAAACTATGAAGAAATGGCACTACTAGATGGGTGTATGATGGG 1168
Db 80 TTTATTACTGGGATCGGCTATCAGGCGCTCCGCTCCACTCACTGGGTTTACGATGGC 139

```


High quality sequence stop: 736.
 Location/Qualifiers
 1. 738
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:5367194"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 94"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
 ORIGIN
 Query Match 11.6%; Score 280.8; DB 12; Length 738;
 Best Local Similarity 63.0%; Pred. No. 2.2e-41;
 Matches 466; Conservative 0; Mismatches 272; Indels 2; Gaps 2;
 QY 748 ATACACTACTGCTTATTCGGACATCATATGTGATATCATCTACCTTTATGATATGCTA 807
 Db 1 ATCCACTTCTGCTCTCATGATTAATCTTGTGGACCTCATCTACCTCTGGACATCACC 60
 QY 808 TTTATCCAGCCAGACTCCAGTTTGTAAAGAGAGAGACATAATAGTAGGATTCAAATGAG 867
 Db 61 GTGTTCCAGATGCGCTCGAG-TTGTCAAAGCGCGGACATCATTCAGACAAGAGGAG 119
 QY 868 CTAAAGAAACACTACAGACTTCTACAAAATTTGATTTGGATGCGCATCAATAATACCA 927
 Db 120 ATGCGTATACTACTCTGAGTCTCGCGGTTTAAAGTAGGACCTGCTGCTCTGCTGCC 179
 QY 928 TTTGATATTGCTACCTCTTCTTTGGGTTTAAATCAATGTTTAAAGCAAAATAGGATGTA 987
 Db 180 TTGACTTCTCTACTTGAACCTTGGCATCAACCTCTCTTCCCTGCGCCGCTGCTG 239
 QY 988 AAGTACACTTCAATTTTGAATTTAATCATCACTAGACTATTAATGGAACAAGATAT 1047
 Db 240 AAGTACATGGCTCTTTTGAATTTAATCAACCGCTTGAAGCCATCTTCAGCAAGCCCTAC 299
 QY 1048 ATCTACAGAGTTATTCGAACAACTGGATCTTGTCTGTTTATTTCTGACATTAATGCTGT 1107
 Db 300 GTTTACAGAGTCATCAGACCAACGCTCTACCTGCTGTACAGCTGCACTCACTCTGCG 359
 QY 1108 GTTTATTAAGCTGCTTCAAACTAAGAGAAATGGCACTACTAGATGGGTGTATGATGGG 1167
 Db 360 CTTTACTACTGGGATCAGCCT-TCCAGGCACTGGCTCCACTCACTGGGTTTACGACGGA 418
 QY 1168 GAAGAAACAGATATCTGAGATGTTATTTATGGCAGTTCCGACTTTTAAATTAATACCATGGT 1227
 Db 419 GTGGGAACAGTTATATTCGATGCTACTAGTGGCTGTGAAACCTCATCAATCATCGGA 478
 QY 1228 GGCCTTCAGAACCAAACTTTATTTGAATTTGTTTTCACACTCTTGAATTTTTTTCT 1287
 Db 479 GGACTGCGGACCCGACAGCCTCTTTGAGATTTGCTTCCAGCTGTGTAATTTTACC 538
 QY 1288 GGAGTTTGTGTTCTCCAGTTTAATTTGTCAGATGAGATGTGATGGAGCAGCTACA 1347
 Db 539 GGGGTCTTGTCTTCTGTGATGATTTGGACAGATGAGATGTTGTTGGGGCGGCCACA 598
 QY 1348 GCCAATCAGAACTACTTCCGCGCTGATGATGACACCAATTCCTACATGAACAATTAC 1407
 Db 599 GCGGGGAGACCTACTACCGCAGCTGATGAGACAGACAGCAGTGAAGTACATGAATCTCTAC 658
 QY 1408 TCATTCCTAACTTGTGCAAAAGCGAGTTTCGACCTTGGTATGAATATATCATGGGACTCT 1467
 Db 659 AAGATCCCAAGTCTGTGCAAGACCGGTGCAAGACCTGGTATGATGATACCTGGCATTCG 718
 QY 1468 CAAGAATGCTAGATGATGTC 1487
 Db 719 CAAGGCATGCTGGATGATGTC 738

RESULT 13

BM938767/c

LOCUS

DEFINITION

BM938767

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

423 bp mRNA linear EST 29-APR-2002
 UI-M-CG0p-bff-f-08-0-UI.r1 NIH BMAP Ret4 S2 Mus musculus cDNA clone
 UI-M-CG0p-bff-f-08-0-UI 5', mRNA sequence.
 BM938767.1 GI:19397914
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 423)
 Ronaldo M.F., Lennon G. and Soares M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 8889548
 Contact: Chin, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mEST@mail.nih.gov
 Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of
 Medicine
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 The following repetitive elements were found in this cDNA
 sequence: 384-411 SPOLY_Asimple_repeat
 Seq primer: M13 REVERSE.
 Location/Qualifiers
 1. 423
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UI-M-CG0p-bff-f-08-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NIH BMAP Ret4 S2"
 /note="Vector: p773D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NIH BMAP Ret4 S2 library is a subtracted library,
 ultimately derived from mouse retina tissue libraries at
 various stages of development. For a detailed description
 of the library from which this clone was derived, please
 visit our web site at brainest.eng.uiowa.edu. The tissue
 for this library was contributed by Dr. Xin-Yuan Fu, Yale
 University School of Medicine"

ORIGIN

Query Match

Best Local Similarity

Matches 322; Conservative

0; Mismatches 70; Indels

0; Gaps

0;

QY

1278

TTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATTTGTCAGATGAGATGATGG 1337

Db

409

TTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATTTGTCAGATGAGATGATGG 350

QY

1338

AGCAGCTACGCCAATCAGAACTACTTCCGCGCTGCATGATGATGATGATGATGATG 1397

Db

349

GGCAGCAACGCCAATCAGAACTACTTCCAGCGCTGCATGATGATGATGATGATGATG 290

QY

1398

GAACAATTAATCTCCATCTCTAACTTGTGCAAAAGCGAGTTCCGGACTTGGTATGAATATAC 1457

Db

289

GAAACAATTAATCTCTCTAACTTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 230

```

QY 1458 ATGGAGCTCTCAAGAATGCTAGATGAGTGTGATTTGCTTTAAGACCTCAACACTACGGT 1517
Db 229 ATGGAAGTCTCAAGAATGCTAGATGAGTGTGATTTGCTTTAAGACCTCAACACTACGGT 170
QY 1518 CCAGTTAGCCCTGCCATTGATGTGACTTACATCATCATCAGCAAGTGTGATTTGCTTCAA 1577
Db 169 GCAGTTGCTTATGTCCTTGCATATAACTTCAGTATCATCGCAAGTGTGATTTGCTTCAA 110
QY 1578 GGGTTGTGATACAGATGATTTATGACATGTTGCTAAGATTTGAAATCCGTTCTCTATT 1637
Db 109 GGGCTGTGACACAGATGATTTATGACCTGCTGCTAAGATTTGAAATCCACTATTATT 50
QY 1638 GCCTGTGATCTTGTCTGCAAAAGGGAGAAA 1669
Db 49 ACCTGGTGACTTTGTCTGCAAAAGGGAGAAA 18

RESULT 14
H53423 H53423 445 bp mRNA linear EST 20-SEP-1995
LOCUS yf86a09.r1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone
DEFINITION IMAGE:231160 5', mRNA sequence.
ACCESSION H53423
VERSION H53423.1 GI:993570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 445)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Ravello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevasakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.,
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
TITLE Contact: Wilson RK
JOURNAL Washington University School of Medicine
MEDLINE 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
PUBMED Tel: 314 286 1800
COMMENT Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 903
High quality sequence stops: 302
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 903 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 302.
Location/Qualifiers
1. 445
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3861151"
/db_xref="taxon:9606"
/clone="IMAGE:231160"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares pineal gland N3HPG"
/note="Organ: pineal gland; Vector: pT73D (Pharmacia)
with a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5', TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTTCTTTT
3'], double-stranded cDNA was size selected, ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of a modified pT733
vector (Pharmacia). Library constructed by Bento Soares
and M.Patina Bonaldo."

```

```

ORIGIN
Query Match 11.5%; Score 279; DB 14; Length 445;
Best Local Similarity 90.1%; Pred. No. 5.4e-41;
Matches 311; Conservative 0; Mismatches 27; Indels 7; Gaps 1;

QY 1 ATGTTTAAATCGCTGACAAAGTCAACAAAGTGAAGCCTATAGGAGAGAAACAATGAGAAT 60
Db 39 ATGTTTAAATCGCTGACAAAGTCAACAAAGTGAAGCCTATAGGAGAGAAACAATGAGAAT 98
QY 61 GAACAAAGTTCTCGTCGGAATGAAGAAGGCTCTCAACCAAGTAAATCACTCTCAGCAAAACC 120
Db 99 GAACAAAGTTCTCGTCGGAATGAAGAAGGCTCTCAACCAAGTAAATCACTCTCAGCAAAACC 158
QY 121 ACAGCACAGGAGAGAAACAAGAGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC 180
Db 159 ACAGCACAGGAGAGAAACAAGAGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC 218
QY 181 ACCTCTGAAGGCCACACCAACATACAAGACAAACTCTCCAAGAAAAATTCCTCTCGA 240
Db 219 AGCTCTGAAGGCCACACCAACATACAAGACAAACTCTCCAAGAAAAATTCCTCTCGA 278
QY 241 GATCTGACCAAAACCTTGACCTCAAAATGAGAGAACCAACTGGACAGTGCAGAG 300
Db 279 GATCTGACCAAAACCTTGACCTCAAAATGAGAGAACCAACTGGAGAACAGTTGCCA 338
QY 301 CAGAAGGAAATCGA-----CCCGCGGAAAGAGGTCCAAACAG 338
Db 339 GAGCAGGAAGGAATGGGACCCCGGGNAAGGAAGTNCACAG 383

RESULT 15
AW465556 545 bp mRNA linear EST 24-FEB-2000
LOCUS BP230019A20H7 Soares normalized bovine placenta Bos taurus cDNA
DEFINITION Clone BP230019A20H7 5', mRNA sequence.
ACCESSION AW465556
VERSION AW465556.1 GI:7035661
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
REFERENCE 1 (bases 1 to 545)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardini,J., Liu,L. and
Larson,J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTACCTCTCACTAAG
Insert Length: 545 Std Error: 0.00
Plate: BP230019A20 row: H column: 7
Seq primer: AGCGGATACAAATTTCCACACAGGA
High quality sequence stop: 545.
Location/Qualifiers
1. 545
/organism="Bos taurus"
source

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2004, 18:22:44 ; Search time 164.746 Seconds
(without alignments)
8185.526 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 atgttaaatcgtgacaaa.....aagaaaagctgaagcaataa 2430

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	93.8	3.9	7218	1	US-08-232-463-14
C 2	85.6	3.5	2223	1	US-08-257-073-4
C 3	78.8	3.2	929	4	US-09-671-317-14
C 4	72.8	3.0	1001	4	US-09-671-317-439
C 5	66.6	2.7	396	4	US-09-640-173-53
C 6	66.6	2.7	396	4	US-09-713-550-53
C 7	66.2	2.7	2394	4	US-09-800-729-33
C 8	65.6	2.7	1696	4	US-09-835-811-1
C 9	65.6	2.7	2447	2	US-09-014-969-14
C 10	64.8	2.7	43795	3	US-08-742-185-101
C 11	64.2	2.6	240	1	US-08-628-417-6
C 12	64	2.6	1447	4	US-08-443-041A-27
C 13	63	2.6	674	4	US-09-620-405B-465
C 14	63	2.6	674	4	US-09-433-826B-465
C 15	63	2.6	674	4	US-09-604-287A-465
C 16	63	2.6	674	4	US-09-834-759-465
C 17	62.8	2.6	1051	3	US-09-245-041-10
C 18	62.6	2.6	118067	4	US-09-497-855A-32
C 19	62.2	2.6	16442	3	US-08-781-891-208
C 20	62.2	2.6	16442	4	US-09-618-166-208
C 21	61.6	2.5	249	4	US-09-621-976-1322
C 22	61.6	2.5	2608	4	US-09-904-615-16
C 23	61.6	2.5	3211	2	US-08-574-959A-8
C 24	61.6	2.5	3211	3	US-09-357-014-8
C 25	61.6	2.5	3901	2	US-08-574-959A-6
C 26	61.6	2.5	3901	3	US-09-357-014-6
C 27	61.4	2.5	282	3	US-09-461-697-205

28	61.4	2.5	306	3	US-09-461-697-203
29	61.4	2.5	696	3	US-09-461-697-193
30	61.4	2.5	699	3	US-09-461-697-191
31	61.4	2.5	717	3	US-09-461-697-189
32	61.4	2.5	774	3	US-09-461-697-187
33	61.4	2.5	819	3	US-09-461-697-185
34	61.4	2.5	1669	3	US-09-461-697-184
35	60.8	2.5	1798	4	US-09-797-906-1
C 36	60.8	2.5	12980	3	US-08-811-566-5
C 37	60.8	2.5	12980	4	US-09-034-756-5
38	60.4	2.5	5394	3	US-08-688-376-1
39	59.6	2.5	240	4	US-09-621-976-1324
C 40	59.6	2.5	5152	4	US-10-204-708-47
41	59.2	2.4	55298	4	US-09-491-356C-1
42	59	2.4	231	3	US-09-461-697-207
43	58.6	2.4	569	4	US-09-461-325-44
44	58.6	2.4	569	4	US-10-012-542-44
45	58.4	2.4	1276	3	US-09-177-325-2

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)833-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptz9pt-F15
; US-08-232-463-14

Query Match 3.9%; Score 93.8; DB 1; Length 7218;

Best Local Similarity 7.3%; Pred. No. 8.9e-14;
Matches 32; Conservative 255; Mismatches 152; Indels 0; Gaps 0;
QY 1874 AAGAAATTCATGATTCAGATTCAGAAAGATTCATGAGAAAGCCAGAGTGC 1933
D 1456 AAGAGATAGAAATTCGATACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1397
QY 1934 TTTTAAAGAGAGCTAAGACCGCAGAGCAACCCCTCCAGAAAGATTCGCCCTCC 1993
D 1396 RRR 1337
QY 1994 TCTTCCACCGAAGAGAGACACCAAACTGTTTAAAACTCTCTAGAGGACAGAA 2053
D 1336 RRR 1277
QY 2054 AAGCAAGCTTCGAGACTACTCAATTTGAAGCAGAGCAAGCAGCTCAGAAAGAAA 2113
D 1276 RRR 1217
QY 2114 ATTCTGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2173
D 1216 RRR 1157
QY 2174 ATAAACAAAAGAAATGAAGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2233
D 1156 RRR 1097
QY 2234 AGCAG 2293
D 1096 RRR 1037
QY 2294 AAGAACCCCACTCAGTTAG 2312
D 1036 TCGGAATTAATTCGTGAG 1018

RESULT 2

US-08-257-073-4
; Sequence 4, Application US/08257073
; Patent No. 5766597
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; APPLICANT: de Taisne, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,073
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,305
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,183
; FILING DATE: 20-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2570
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-257-073-4
Query Match 3.5%; Score 85.6; DB 1; Length 2223;
Best Local Similarity 68.6%; Pred. No. 6.1e-12;
Matches 118; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 2088 AGAGCAAGCAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2147
D 2016 AATAG 2075
QY 2148 TGAAGATAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2207
D 2076 AGAAG 2135
QY 2208 AATAG 2259
D 2136 AGAAG 2187

RESULT 3

US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-363 : polymorphic base A or G
; NAME/KEY: misc.binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-363.mis1, potential
; NAME/KEY: misc.binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-454-363.mis2, potential complement
; NAME/KEY: primer.bind
; LOCATION: 139..158
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer.bind
; LOCATION: 634..652

```

; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-454-363 potential probe
; NAME/KEY: misc_feature
; LOCATION: 674..679,881..882,892..893
; OTHER INFORMATION: n=a, g, c or t
US-09-671-317-14

Query Match          3.2%; Score 78.8; DB 4; Length 929;
Best Local Similarity 63.7%; Pred. No. 2.1e-10;
Matches 116; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY      2061 TCTTGCACGACTACTCAATTGAAGCGAGACCAAGCAGCTCAGAAGAAAGAAAATTTCTGA 2120
           ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       919 TCACGCCATTGGCACTCCAGCTTGAGCNCNCCAGCGANNCCATCTCAAAGAAAGAAAGA 860
           ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      2121 AGGAGGAGAGGAGAAAGGAAAAAAGAAAAATCAAGATAAACAAAAAGAAAATGAAGATAAAC 2180
           ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       859 AGRAGAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 800
           ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      2181 AAAAGAAAATGAAGATAAAGGAAAAAAGAAAATGAAGATAAAGATAAAGGAAGAGACCAGA 2240
           ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       799 AGAAGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 740
           ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      2241 AG 2242
           |||
Db       739 AG 738

RESULT 4
US-09-671-317-439/c
; Sequence 439, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLSLIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62 US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 439
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-242 : deletion AT
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-242.misl, potential
; NAME/KEY: primer_bind
; LOCATION: 260..279
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 755..773
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_feature
; LOCATION: 795..800
; OTHER INFORMATION: n=a, g, c or t

```

```

; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713,550-53

```

[illegible]

RESULT 7

```

US-09-800-729-33
; Sequence 33, Application US/09800729
; Patent No. 660592
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: 32 Human secret
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/8
; CURRENT FILING DATE: 2001-03-08
; PRIORITY APPLICATION NUMBER: PCN/US00
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,7
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 2394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-33

```

Query Match	2.7%	Score 66.2;	DB 4;	Length 2394;
Best Local Similarity	60.1%;	Prod. NO. 5.4e-07;		
Matches 110;	Conservative 0;	Mismatches 73;	Indels 0;	Gaps 0;
2064 QY	TGCAAGACTACTCAAAATTGAAGCGAGCAGACGACTCAGACGAAAGAAATTC	TGAAGG	2123	
2188 Db	TTCAAGAAATCCATAAAGGAAGGACGGTAACCTTATGATACAAAAA	AAAAAAAAAAAA	2247	
2124 QY	ACGACAGCAACAGACGAAAAAGAAATCAACATATAACAAAAAGAAATGAAGATAAACAAAA	CAAAAA	2183	
2248 Db	AAAAAGCAAAAGAGAAAAA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2307	
2184 QY	AGAAATGAAGATTAAGGAAAGAAATGAAGATTAAGATTAAGGACAGAGCCAGAGA		2243	
2308 Db	AA	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2367	

QY	2244	GAA	2246
Db	2368	AAA	2370

RESULT 8

```

US-09-835-811-1
; Sequence 1, Application US/09835811
; Patent No. 6482936
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: US$ THEREOF
; FILE REFERENCE: CL0012228
; CURRENT APPLICATION NUMBER: US/09/835,811
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
US-09-835-811-1

```

Query Match	2.7%	Score 65.6;	DB 4;	Length 1696;
Best Local Similarity	56.5%;	Prod. No. 6.4e-07;		
Matches 122;	Conservative 0;	Mismatches 94;	Indels 0;	Gaps 0;
QY	2031	AACCTCTCTAGGAGGCACAGGAAACCAAGTCTTGCAGAGCTACTCTCAATTTGAAGCCGAGA	2090	
Db	1472	ACCTGTCCCCCTCCCAAGATTAAAGATCACTGTATAGATTAAATAAAAAAAAAAAAAA	1531	
QY	2091	GCAAGCAGCTCAGAGAGAAAGAAATTTCTCGAGGAGGAGCAGAGAGAAAGAAATGA	2150	
Db	1532	AA	1591	
QY	2151	AGATATACAAANACAAANTCAGAGATAACACAAAGAGAAATGAAGATTAAGGARAAGAAA	2210	
Db	1592	AA	1651	
QY	2211	TCAAGATAAAGATAAAGGAGAGAGCCAGAGAGAA	2246	
Db	1652	AA	1687	

RESIST. 9

```

US-09-014-969-14
; Sequence 14, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,969
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-09-014-969-14

Query Match 2.7%; Score 65.6; DB 2; Length 2447;
Best Local Similarity 56.0%; Pred. No. 7.7e-07;
Matches 122; Conservative 1; Mismatches 95; Indels 0; Gaps 0;

Qy 2029 AAAAATCTCTAGAGCCACAGGAAAGCAAGTCTTGCAGACTACTCAAAATTTGAAGCGA 2088
Db 2229 ATAAACCTTTTGGGAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2288
Qy 2089 GAGCAACGAGCTCAGAGAAAGAAAATTTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAG 2148
Db 2289 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2348
Qy 2149 GAAGATTAACAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAAGGAAAGAA 2208
Db 2349 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2408
Qy 2209 AATCAAGATTAAGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2246
Db 2409 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2446

RESULT 10
US-08-742-185-101
; Sequence 101, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,734
; FILING DATE: 31-JUL-1996

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,429
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-742-185-101

Query Match 2.7%; Score 64.8; DB 3; Length 43795;
Best Local Similarity 63.5%; Pred. No. 4.9e-06;
Matches 99; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 2087 GAGAGCAAGCAGCTCAGAGAAAGAAAATTTCTGAAGGAGGAGGAGGAGGAGGAGGAGGAG 2146
Db 38894 GAGATGAGAGAAAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 38953
Qy 2147 ATGAGATTAACAAAGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAAGGAAAG 2206
Db 38954 AGGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39013
Qy 2207 AAAATCAGATTAAGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2242
Db 39014 AAGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39049

RESULT 11
US-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESSEE: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid
```


[illegible]

QY	2228	GAA	2230
Db	672	AAA	674

RESULT 15

```

US-09-604-287A-465
; Sequence 465, Application US/09604287A
; Patent No. 8586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 465
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-465

```

Query Match	2.6%;	Score 63;	DB 4;	Length 674;
Best Local Similarity	59.0%;	Pred. No. 1.9e-06;		
Matches 108;	Conservative 0;	Mismatches 75;	Indels 0;	Gaps 0;

Qy	2048	CAGGAAAGCAAGTCTTTCGAAGACTACTCAAATTGAAGCGAGACGACGCTCAGAAGA	2107
Db	492	CAGCAAAAGGAGACCTTAGGAGATCCATCGGAGAAAAGATGACTCAGTTAAGGCAA	551
Qy	2108	ARGAAATTTCTGAAGAGGAGCAGGAAGAGAAAAGAAATGAAGATAAACAAAAAGAAA	2167
Db	552	AA	611
Qy	2168	ATGAAGATAAACCAAAAAAGAAAATCAAGATAAAGGAAAAAGAAATGAAGATAAAGATAAG	2227
Db	612	AA	671
Qy	2228	GAA	2230
Db	672	AAA	674

Search completed: June 22, 2004, 04:09:27
Job time : 167.746 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2004, 00:29:50 ; Search time 994.629 Seconds
(without alignments)
11192.162 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 agtcttaaatcgctgacaaa.....aagaaaagctgaagcaataa 2430

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	577.4	23.8	2607	16	US-10-189-507-3
2	577.4	23.8	4382	16	US-10-159-563-147
3	306	12.6	680	13	US-10-027-632-204539
4	306	12.6	680	13	US-10-027-632-204539
5	176.4	7.3	2500	13	US-10-342-887-427
6	176.4	7.3	2500	13	US-10-172-118-427
7	133.2	5.5	3027	15	US-10-295-573-1
8	132.8	5.5	2085	15	US-10-345-680-27
9	132.8	5.5	3494	15	US-10-345-680-25
10	131.6	5.4	1995	15	US-10-087-217-1
11	131.6	5.4	1995	15	US-10-087-217-5
12	131.6	5.4	3027	15	US-10-295-573-2
13	131.6	5.4	3027	15	US-10-295-573-4
14	129	5.3	526	9	US-09-864-761-12975

15	128.4	5.3	1995	15	US-10-087-217-3	Sequence 3, Appli
16	128.4	5.3	1995	15	US-10-087-217-7	Sequence 7, Appli
17	128	5.3	2877	15	US-10-295-573-3	Sequence 3, Appli
18	127	5.2	127	9	US-09-864-761-29538	Sequence 29538, A
19	111.2	4.6	1995	9	US-09-735-927-1	Sequence 1, Appli
20	111.2	4.6	1995	14	US-10-034-843-1	Sequence 1, Appli
21	111.2	4.6	1995	15	US-10-168-651-34	Sequence 34, Appli
22	111.2	4.6	1995	16	US-10-189-507-1	Sequence 1, Appli
23	111.2	4.6	2111	15	US-10-114-153-17	Sequence 17, Appli
24	111.2	4.6	2190	15	US-10-029-677-23	Sequence 23, Appli
25	111.2	4.6	12017	9	US-09-735-927-3	Sequence 3, Appli
26	109.6	4.5	1995	16	US-10-189-507-4	Sequence 4, Appli
27	109.6	4.5	2186	15	US-10-029-677-1	Sequence 1, Appli
28	84	3.5	31124	13	US-10-087-192-463	Sequence 463, App
29	81	3.3	625	13	US-10-027-632-179350	Sequence 179350,
30	81	3.3	625	16	US-10-027-632-179350	Sequence 45, Appl
31	80	3.3	2232	15	US-10-087-464-45	Sequence 19262, A
32	79.6	3.3	305	9	US-09-864-761-19262	Sequence 2534, Ap
33	79.6	3.3	496	9	US-09-864-761-2534	Sequence 49, Appl
34	79.2	3.3	37265	13	US-10-087-192-49	Sequence 313, App
35	79.2	3.3	39443	16	US-10-085-117-3113	Sequence 20595, A
36	79	3.3	276	9	US-09-864-761-20595	Sequence 3829, Ap
37	79	3.3	462	9	US-09-864-761-3829	Sequence 3, Appli
38	79	3.3	1728	9	US-09-927-267-3	Sequence 2, Appli
39	79	3.3	1728	16	US-10-189-507-2	Sequence 2, Appli
40	79	3.3	2308	9	US-09-927-267-2	Sequence 351, App
41	79	3.3	2366	13	US-10-302-172-351	Sequence 29, Appl
42	79	3.3	2551	10	US-09-842-758-29	Sequence 29, Appl
43	79	3.3	2551	13	US-10-174-333-29	Sequence 14, Appl
44	78.8	3.2	929	13	US-10-234-334-14	Sequence 15, Appl
45	78.6	3.2	143899	10	US-09-972-546-15	

ALIGNMENTS

RESULT 1

- US-10-189-507-3
- Sequence 3, Application US/10189507
- Publication No. US20030228633A1
- GENERAL INFORMATION:
- APPLICANT: ZOLLER, MARK
- APPLICANT: XU, HONG
- APPLICANT: STASZEWSKI, LENA
- APPLICANT: MOYER, BRYAN
- APPLICANT: PRONIN, ALEX
- APPLICANT: ADLER, JON ELLIOT
- APPLICANT: SALLAMANT, GUY
- APPLICANT: CALLAMARAS, NICHOLAS
- TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
- TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
- TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
- TITLE OF INVENTION: SMELL MODULATORS
- FILE REFERENCE: 078003-0291567
- CURRENT APPLICATION NUMBER: US/10/189,507
- CURRENT FILING DATE: 2003-02-12
- PRIOR APPLICATION NUMBER: 60/303,140
- PRIOR FILING DATE: 2001-07-06
- PRIOR APPLICATION NUMBER: 60/337,154
- PRIOR FILING DATE: 2001-12-10
- NUMBER OF SEQ ID NOS: 12
- SOFTWARE: PatentIn Ver. 2.1
- SEQ ID NO 3
- LENGTH: 2607
- TYPE: DNA
- ORGANISM: Homo sapiens
- US-10-189-507-3

Query Match 23.8%; Score 577.4; DB 16; Length 2607;
Best Local Similarity 64.3%; Pred. No. 8.4e-119;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;
QY 617 TTCCAACAGCATAGATTACACAGATCGACTCTATCTCTGTGGCTTGTGTCGA 676

Db 782 TTCCCGCAGCATGACCGCTGACCAACCTGATGTATGCTCTATGCTGTCTCTGCTGG 841
Qy 677 CTCCTGCTCTAATCGAAGCTGCTGTTTATACCACTGCGCTCTCTTCCCATATCAA 736
Db 842 TGATGCGCTGGAATTTGGAACCTGTTGGCTGATTCGCGTGGCGCTTCCCTTACCAGA 901
Qy 737 CGCAGACAAATACACTACTGCTGCTATTGCGGACATCATATGATGATATCATCTACCTTT 796
Db 902 CCCGGAACAATCCACACCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 961
Qy 797 ATGATATGCTATTTATCCAGCCCAAGCTCCAGTTTGAAGAGGAGAGACATATATGAG 856
Db 962 TGGACATACCGCTGTTCCAGACAGCCCTGCACTGTTGTCAGAGGCGGAGACATCATACGG 1021
Qy 857 ATTCGAATGAGTAAAGAAACATACAGGACTTCTACAAATTTCACTTGGATGCTCCAT 916
Db 1022 ACAAAGGACATCGGAATTAACCTACCTGAACTCTCGCGCTTCAAGATGACCTGCTCA 1081
Qy 917 CAATAATACCAATTTGATATTTGCTACCTCTTTTGGGTTTAAATCCAAATGTTAGACAA 976
Db 1082 GCCTCCTGCCCTTGGATTTCTATTTGAAAGTCGGTGTGAACCCCTCTCTCGCGCTGC 1141
Qy 977 ATAGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCATCACTAGAGCTATAATGG 1036
Db 1142 CCCGCTGTTAAAGTACATGCGCTTCTTCGAGTTTAAACAGCGCTGGAATCCATCTCA 1201
Qy 1037 ACAAGACATATATACAGAGTTATTGAAACAACTGGATCTTCTCTGTTTATTTCTGCACA 1096
Db 1202 GCAAGCCTACGTTACAGGCTCATCAGGACCAAGCTACCTTCTCTACAGCTGCTCAT 1261
Qy 1097 TTAATGCTGTTTATTTACTGGGCTTCAAACTATGAAGAAATGGCACTACTAGATGGG 1156
Db 1262 TGAATTCCTGCTTTTACTGGGCTGCGCTATCAGGCGCTCGGCTCCACTCACTGGG 1321
Qy 1157 TGTATGATGGGAGGAAACAGATCTGAGATGTTATTGCGAGTTTAAATGGCACTTTAA 1216
Db 1322 TTTAGATGGGAGGAAACAGATTTATTCGCTGTTACTACTTGTGTTGTAAGACCTCA 1381
Qy 1217 TTACATTTGGGCTTCCAGAAACCAAACTTTTATTGAAATTTGTTTCAACTCTGA 1276
Db 1382 TCACCATCGGGGGCTGCTGACCCCAAGACACTCTTTGAAATTTGCTTCCAGCTGCTGA 1441
Qy 1277 ATTTTCTGCTGAGTTTCTGTTGTTTCTCCAGTTTAAATGCTCAGATGAGAGTGTATTG 1336
Db 1442 ATTTTCTCAGCGGCTCTTCTGCTTCTGATGATCGGACATGAGAGATGTTGTAG 1501
Qy 1337 GAGCAGCTACAGCAATCAGAACTACTTCCGCGCTGCTGATGATGACCACTTGCCTACA 1396
Db 1502 GGGCGCCACCGCGGACAGACCTTACCGCAGCTGATGGACAGCAACGTTGAAGTACA 1561
Qy 1397 TGAACAATTACTCTTAATCTTAACTTTGTAAGAGGAGTTGCGAGTTGATGATATA 1456
Db 1562 TGAATTTCTACAAGATCCCAAGTCCGTTGCGAAGAACCGCGTCAAGACCTGTGATGAGTACA 1621
Qy 1457 CATGGACTCTCAAGAATGCTAGATGATGCTGATTTGCTTAAGACCTTCAACACTACGG 1516
Db 1622 CTTGGCACTCGAAGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1681
Qy 1517 TCCAGTTAGCCCTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1576
Db 1682 TCGGCTGGACCTCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1741
Qy 1577 AGGTTGTGATACAGATGATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1636
Db 1742 AGGCTGTGACCGGAGATGATCTTTGACATGCTGAAGGCTTGGCTCTGTTGTTCTACC 1801
Qy 1637 TGCTGTGATCTTTGTTGCAAAAGGAGAAATTTGGCAAGGAAATGATATCATCAAGC 1696
Db 1802 TGCCCAACAGCTATGTTGCAAGAGGAGGAGATCGGCGCTGAGATGATCATCATCAGG 1861
Qy 1697 ATGAGAGATCCAAAGTTCTTGGAGCGCTGATGATGATGATGATGATGATGATGATGATGAT 1756

Db 1862 CAGGCAAGTGCAGCTTCTGGCGGCCCTGATGGAAATCTCTGCTGCTGACCTGAAAG 1921
Qy 1757 CTGGGTCGGTGTTCGAGAAATCAGCTTCTAGCAGCAGGAGGAGAAACCTCGAACTG 1816
Db 1922 CTGGATCTGTGTTGAGAAATAGCTTGTGCTGCTGTTGGGCGGGAACCGGCGACGG 1981
Qy 1817 CCAATGTGTGTCGCCACCGGTTTGCAATCTTTTAACTCTAGACAAAAGACCTTCCAAG 1876
Db 1982 CCAACGTGTGTCGCCACCGGTTTACCAACCTCTTCTCATCTGATAGAAGACCTGAATG 2041
Qy 1877 AAATCTAGTGAATTCAGATTTCTGAAGATCTCATGAAGAACCCAGAGTGTCTTT 1936
Db 2042 AGATTTGTGATGATTTCTGATCTCAGAAGTTTACTCCGAAGAAACCCAGGCGCATGC 2101
Qy 1937 TAAAGCAGAGGCTAAGACCGCAGAG 1963
Db 2102 TGAAGACNACATTAAGCCCAAGAGG 2128

RESULT 2

US-10-159-563-147
; Sequence 147, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 4382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-147

Query Match 23.8%; Score 577.4; DB 16; Length 4382;
Best Local Similarity 64.3%; Pred. No. 1.1e-119;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

Qy 617 TTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTGTGGCTTTGCTTTGTCA 676
Db 1983 TTCCCCAGAGCATTCACCCGCTGACCAACCTGATGTATGCTCTATGGCTGTTCTGGTG 2042
Qy 677 CTCCTTGCCTTAACCTGGAACCTGCTGGTTTATACCACTGCGCTCTCTCCCATATCAA 736
Db 2043 TGATGGCTTGGAAATTTGGAACCTGTTGGCTGATTCGCGCTGCGCTTCCCTTACCAGA 2102
Qy 737 CGCAGACAAACATACACTACTGCTGCTTATTGGGACATCATATGATGATATCATCTTT 796
Db 2103 CCCCGAGACATCCACCACTGGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 2162
Qy 797 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGAAGAGGAGGAGACATATAGTGG 856
Db 2163 TGGACATCACCGTGTTCAGACACGCTGCAAGTTTGTTCAGAGGCGGAGACATATACGG 2222
Qy 857 ATTCAAATGAGCTAAGGAAACACTACAGGACTTCTTACAAAATTTTCAGTTGATGTCGAT 916
Db 2223 ACAAAGGACATGCGAATTAACCTACCTGAAGCTCTCGCGCTTCAAGATGACCTGCTCA 2282
Qy 917 CAATTAATACCAATTTGATATTTGCTACCTCTCTTTGGGTTTAAATCCAAATGTTAGACAA 976
Db 2283 GCCTCTGCTTGGATTTCTCTATTTGAAGTCGGTGTGAACCCCTCTCTCCGCTGC 2342
Qy 977 ATGAGATGTTAAAGTACACTTCAATTTTGAATTTAAATCATCACCTAGAGTCTATAATGG 1036

1345	ACAGCCAAATCAGAACTACTTTCGCGCCCTGCATGGATGACACCACTTGCCTACATGAACAAT	1404
1480	AATGCCACACGACGACGAGTTCCAGGCGAAAGATTGATGCTGTCAAACTACATGCAAGTTC	1539
1405	TACTCCATTCCCTAACTTGTGFCAAAACGAGTTCGGACTTGGTATGAATATACATGGGAC	1464
1540	CGAAAGGTGAGCAAAAGACATGGAGCGCAAGGTCATCAAATGTTTGTACTACTTGTGGACC	1599
1465	TCTCAAAGAAATCTAGATCAGTCTGATTTTGTCTTAAGACCCCTACCAACTACGGTCCAGTTA	1524
1600	AATAAGAAGACAGTAGATGAACGAGAGTCTCAAGAACCTGCCAGCAAGCTCAGGGCT	1659
1525	GCCTCGCCAAATGATGTGAACTTCAGCATCATCAGCAAAAGTCGACTTGTCAAGGGTTGT	1584
1660	GAGATAGCCAAATTAATGTTTCACATTGTCCACTCTCAAGAAAGTCGCATATTTCCAGGATTGT	1719
1585	GATACACAGATGATTATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTGTCCTGGT	1644
1720	GAGCTGGCTACTGGTGGAACTGGTACTGAAGCTTCGCTCTCAGGTCCTTAGTCTTGA	1779
1645	GACTTTGTCTGCAAAAGGAGAAATTTGGCAAGGAAATGTATATCATCAAGCATGGAGAA	1704
1780	GATTATATTTGCGGTAAAGGGGACATTTGGCAAGGAAATGTACATCATCAAGGAGGCAAG	1839
1705	GTCCAAAGTCTTGGAGGCCCTCATGGTACTAAAGTTCTTGGT---TACTCTGAAAGCTGG	1760
1840	TTGGCAGTGGTAGCTGATGATGGCGTGACTCAGTATGCGTTGCTCTCAGCTGGAGCTGC	1899
1761	GTCCGTGTTTGGAGAAATCAGCCTTTCTAGCAGCAGGAGGA--GGAAACCGTCAACTGCC	1818
1900	TTTGGTGAGATTAGTATCCTTAACATTAAAGGGTAGCAAAATGGGCAATCGACGTACTGCT	1959
1819	ATGTGGTGCCACGGGTTTGCCCAATCTTTTAACCTTAGACAAAGAACCCCTCAAGAA	1878
1960	AATATCCGTAGCTCGGGCTACTCAGATCTCTTCTGCTTGTCCAGGACGATCTTATGGAA	2019
1879	ATTCTAGTGCANTATCCAGATTCTCAAAAGGATCCCTCATCAAGAAAGCAGAGTGCCTTTA	1938
2020	GCTGTAACGTGAGTATCCTGATGCCAAGAGGTCCTGGAGGACGGGTAGGAGATCCTG	2079
1939	AGCAGAAAGGCT	1950
2080	ATGAAGATGGGT	2091

RESULT 8

US-10-345-680-27

; Sequence 27, Application US/10345680

; Publication No. US20030148394A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: Silos-Santiago, Immaculada

; APPLICANT: Venkateswarlu, Karicheti

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 2527

; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,

; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLEC

; FILE REFERENCE: MPI02-012PIRNM OMNI

; CURRENT APPLICATION NUMBER: US/10/345,680

; CURRENT FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/349,511

; PRIOR FILING DATE: 2002-01-18

; PRIOR APPLICATION NUMBER: US 60/360,500

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/365,041

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: US 60/374,063

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: US 60/403,468

; PRIOR FILING DATE: 2002-08-14

; PRIOR APPLICATION NUMBER: US 60/414,262

; PRIOR FILING DATE: 2002-09-27

; PRIOR APPLICATION NUMBER: US 60/419,986

```

; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2085
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2085)
; US-10-345-680-27

Query Match          5.5%; Score 132.8; DB 15; Length 2085;
Best Local Similarity 49.2%; Pred. No. 3.3e-19;
Matches 487; Conservative 0; Mismatches 472; Indels 31; Gaps 4;

QY      856 GATTCAATGAGCTAAGGAAACACTACAGGACTTCTCAAAAATTTTCAGTTGCATGTCGA 915
Db      703 GATACCAACAGCGTGTGGCAGCATTAACAAGACGACCACGAGTTCAAGCTGGATGTGTG 762
QY      916 TCATAATATACCAATTTGCATATTTGCTACCTCTCTTTGGGTTTA---ATCCAATGTTTGA 972
Db      763 TCCTGTGTCGCCACCGACTGCTGCTTACTTAAAGTGGGCACAACTACCACGAGTGAGG 822
QY      973 GCAAAATAGAGTGTAAAGTACACTTCATTTTTTGAATTTAATCATCACTACCTAGAGTCTATA 1032
Db      823 TTCACCGCGCTACTGAAGTTTCCCGGCTCTTTGAATTTCTTCCCGCACAGACACAAGG 882
QY      1033 ATGGCAAAAGCATATATCTACAGAGTTATTCGACAACTGGATCTGCTGTTTATTCTG 1092
Db      883 ACCAACTACCCCAATATGTTCCAGATTTGGGAATCTGGTCTGTGTACATTTCTCATCATC 942
QY      1093 CACATTAATGCTGTGTTTATTACTGGGCTTCAAATATGAAGGAATTCGGCACTACTAGA 1152
Db      943 CACTGGATGCGTGCATCTACITTTGCCATTTCCAACTTCAATGGTTTGGGACAGACTCC 1002
QY      1153 TGGGTGT-----ATGATGGGGAAGGAACAGGATCTGAGA 1188
Db      1003 TGGGTCTACCCAAACATCTCAATCCAGAGCATGGCGGCTCTCCAGGAAGTACATTTAC 1062
QY      1189 TGTATTATTGGGCAGTTCGAATTTAAATACCATTGGTGGCCTTCCAGAACCAACAATCT 1248
Db      1063 AGTCTCTACTGCTCCACCTTGACCTTACCACATTTGAGACACCCACCCCGGTGAAA 1122
QY      1249 TTATTTGAAATGTTTTTCAACTCTTGAATTTTTTTCTGGAGTTTCTGTTCTCCAGT 1308
Db      1123 GATGAGAGTAUCTCTTTTGTGTCGTAGACTTCTTGTGGGTGTTCTGATTTTGGCACCC 1182
QY      1309 TTAATTTGTCAGATGAGAGATGATTTGGAGCAGCTACAGCAATCAGAACTACTTCCGC 1368
Db      1183 ATTGTGGGCAATGTGGCTCCATGATCTCGAATATGAATGCTTCACGGGACGAGTTCCAG 1242
QY      1369 GCCTGCTGATGACACCACTTGGCTACATGAACAATTTACTCCATTTCTAAACTTGTGCAA 1428
Db      1243 GCCAAGATTGATTCATCCATCAAGCAGTACATGCAGTTCCGCAAGTCCCAAGGACTTGGAG 1302
QY      1429 AAGGAGTTCCGACTTGGTATGATATATACATGGGACTCTCAAGATGCTAGATGAGTCT 1488
Db      1303 ACGGGGTTATCCGGTGGTTTGAATCTACCTGTGGGCCAACCAAGGAAGCGGTGGATGAGAG 1362
QY      1489 GATTTGCTTAAGACCCCTTACCACACTACGGTCCAGTTAGCCCTCCGCAATTTGATGTGAATCTC 1548
Db      1363 GAGGTGCTCAAGAGCTTCCACAGACAGCTGAAGGCTGAGATCGCCATCAACGTGCACCTG 1422
QY      1549 AGCATCATCAGAAAGTCGACTTGTTCAGGGTTGTGATACACAGATGATTTATGACATG 1608
Db      1423 GACACGCTGAAGAAGGTTCCGATCTTCCAGGACTGTGAGGACAGGCTGCTGGTGGAGCTG 1482
QY      1609 TTGCTAAGATTGAATCCGTTCTCTATTTCCTTGGTGACTTTTCTGTGCAAAAAGGAGAA 1668
```

RESULT 9

```
US-10-345-680-25
; Sequence 25, Application US/10345680
; Publication No. US20030148394A1
```

GENERAL INFORMATION:

```
; APPLICANT: Millennium Pharmaceuticals, Inc.
```

```
; APPLICANT: Silos-Santiago, Immaculada
```

```
; APPLICANT: Venkateswarlu, Karicheti
```

```
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
```

```
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
```

```
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
```

```
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
```

```
; FILE REFERENCE: MF102-012PIRNM OMNI
```

```
; CURRENT APPLICATION NUMBER: US/10/345,680
```

```
; CURRENT FILING DATE: 2003-01-16
```

```
; PRIOR APPLICATION NUMBER: US 60/349,511
```

```
; PRIOR FILING DATE: 2002-01-18
```

```
; PRIOR APPLICATION NUMBER: US 60/360,500
```

```
; PRIOR FILING DATE: 2002-02-28
```

```
; PRIOR APPLICATION NUMBER: US 60/365,041
```

```
; PRIOR FILING DATE: 2002-03-15
```

```
; PRIOR APPLICATION NUMBER: US 60/374,063
```

```
; PRIOR FILING DATE: 2002-04-19
```

```
; PRIOR APPLICATION NUMBER: US 60/403,468
```

```
; PRIOR FILING DATE: 2002-08-14
```

```
; PRIOR APPLICATION NUMBER: US 60/414,262
```

```
; PRIOR FILING DATE: 2002-09-27
```

```
; PRIOR APPLICATION NUMBER: US 60/419,986
```

```
; PRIOR FILING DATE: 2002-10-21
```

```
; PRIOR APPLICATION NUMBER: US 60/423,809
```

```
; PRIOR FILING DATE: 2002-11-05
```

```
; PRIOR APPLICATION NUMBER: US 60/429,797
```

```
; PRIOR FILING DATE: 2002-11-26
```

```
; NUMBER OF SEQ ID NOS: 66
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 25
```

```
; LENGTH: 3486
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo Sapiens
```

```
; FEATURE:
```

```
; NAME/KEY: CDS
```

```
; LOCATION: (40)...(2124)
```

```
; US-10-345-680-25
```

Query Match 5.5%; Score 132.8; DB 15; Length 3486;

Best Local Similarity 49.2%; Pred. No. 4.4e-19;

Matches 487; Conservative 0; Mismatches 472; Indels 31; Gaps 4;

QY 856 GATTCAATGAGCTAAGGAAACACTACAGGACTTCTCAAAAATTTTCAGTTGCATGTCGA 915

Db 742 GATACCAACAGCGTGTGGCAGCATTAACAAGACGACCACGAGTTCAAGCTGGATGTGTG 801

QY 916 TCAATAATACCAATTTGATATTGCTACCTCTCTTTGGGTTTA---ATCCAATGTTTGA 972

Db 802 TCCCTGGTCCCCACCGACTGGCTTACTTAAAGTGGGCACAACTACCCAGAGTGAAG 861

QY 973 GCAAAATAGAGTGTAAAGTACACATTTTCAATTTTGAATTTAATCATCATCCTAGAGTCTATA 1032

1561	TTTGGTGAGATTAGTATCCTTAACTTAAGGGTAGCAAAATGGCAATCGACGTACTGCT	1620
Db		
1819	AATGTGGTGCCACCGGGTTGGCAATCTTTTAACTCTAGACAAAAAGACCCCTCCAGAA	1878
Qy		
1621	AATATCGTAGCTGGGCTACTCAGATCTCTCTGTCTGTCCAAGGACGATCTATCGAA	1680
Db		
1879	ATTCTAGTGCAATTATCCAGATTCTGAAGATCCTCATGAAGAAAGCCAGAGTCTTTTA	1938
Qy		
1681	GCTGTAACTCAGTATCCTGTATGCCAAGAGGTCTCTGGAGGAACGGGGTAGGGAGATCCTG	1740
Db		
1939	AAGCAGAAAGGCT	1950
Qy		
1741	ATGAAGATGGGT	1752
Db		

```

RESULT 12
US-10-295-573-2
; Sequence 2, Application US/10295573
; Publication No. US20030157571A1
; GENERAL INFORMATION:
; APPLICANT: Karpen, Jeffrey W.
; APPLICANT: Rich, Thomas C.
; APPLICANT: Cooper, Dermot M.F.
; APPLICANT: Schaack, Jerome
; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS
; FILE REFERENCE: UTC-07536
; CURRENT APPLICATION NUMBER: US/10/295,573
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/332,494
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 3027
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-295-573-2

```

Query Match	5.4%;	Score 131.6;	DB 15;	Length 3027;
Best Local Similarity	46.7%;	Pred. No. 7.6e-19;		
Matches 622;	Conservative	0;	Mismatches 674;	Indels 36; Gaps 5;
QY	652	TATCTCCTCTGGGCTCTTGCTTGTCATCTCTGCTTAACACTGGAACCTGCTGGTTTATACCA	711	
DB	763	TATTAACCGTTGGTTGTTTGTTCATTGCGCATGCGCTGTTCTTTACAACCTGGTGCCTGTTGGTG	822	
QY	712	CTGGCGCTCGTCTTCCCATATCAACCGGAGAGCAACATACACTACTGCTGCTTATTCGGGAC	771	
DB	823	GCGAGAGCTGCTTCAGTGATCTACAGAGAACTATTGTGGTATGGCTGGTGCCTGGAC	882	
QY	772	ATCATATGTGATATCATCTACCTTTTATGATATGCTATTTATCCAGGCCAGACTCCAGTTT	831	
DB	883	TACTTCTCAGACACTGCTATATCGAGAGACCTCATCATTCGGCTGGCGCACAGGC---	939	TTT
QY	832	GTAAGAGGAGGAGACATAATAGTGGATTCAAATGAGCTAAGAAACACTACAGGACTTCT	891	
DB	940	CTAGAACAGGGGCTCTTGTCTAAGATCCAGAAATTCGGAGACAACATATTCACACT	999	
QY	892	ACAAATTTTCAGTTGATGTGGCATCAATAATACCATTTGATATTTGCTACCTCTTCTTT	951	
DB	1000	TTGCAGTTCAAATTTGATGTGGCTTCTATCATTTCCCACTGACCTATCTATTTTGCTGTG	1059	
QY	952	GGGTT---TAATCCAAATGTTTAGAGCAAAATAGATGTTAAAGTACACTTCATTTTTTGAA	1008	
DB	1060	GGTATCCACAGCCCTGAGGTACGCTTCAACCGTCTATTACACTTTGCCGTATGTTGAG	1119	
QY	1009	TTTAATCATCCTAGAGTCTATAATGGACAAGCATATATCTACAGAGTTATTCGAACA	1068	
DB	1120	TTCTTTGACCGGACTGAGACACGACACAGCTACCCCAACATCTTCGGAATCAGCAATCTG	1179	
QY	1069	ACTGGATACTTTCGTGTTTATTCTGCACATTAATGCGCTGTGTTTATTACTGGGCTTCAAC	1128	

Db	1180	GTCTTTACATCTTTGGTCATCATCCACTGGAATGCTTGTATTTATTTATGTTATTTCTTAAG	12339
Qy	1129	TATGAAGGAATTGG-----CACTACTAGATGGGTGTATGAT	1164
Db	1240	TCCATTGGCITTTGGAGTTGACACCTGGTTTACCCCAACATTACTGACCTGAATATGGC	1299
Qy	1165	GGGAAGGAACGAGTATCTGAGATGTTATTTATGGCAGTTCGAACTTTAAATTAACCAATT	1224
Db	1300	TACCTGGCTAGAGAGTACATTTACTGTGCTTTACTGTGTCCACACTGACCCCTCAACCACT	1359
Qy	1225	GGTGGCCTTCAGAACCAACAAATTTTATTTGAAATGTTTTTCAACTCTTTGAATTTTTTT	1284
Db	1360	GGAGAGACACACCCCTGTAAAGGATGAGAGTACCTATTGTGTCACTCTTGTACTCTCTG	1419
Qy	1285	TCTGGAGTTTTTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGAGATGTGATTTGAGCAGCT	1344
Db	1420	ATTGGTGTCTCTCATCTTTTGGCACTATTGTGGGAAATGTGGGCTCCATGATCTCCAACTG	1479
Qy	1345	ACAGCCAAATCAGAACTACTTTCGGCGCTGCATCGGATGACACCAATTCGCTACATGAACAAT	1404
Db	1480	AATCCACACGACGAGAGTTCCAGGCCAAGATTGATGCTGTCAAACACATACATGCAAGTTC	1539
Qy	1405	TACTCCATTTCCTAAACTTGTGCAAAACGAGTTCGGACTTGTGATGAATATACATGGGAC	1464
Db	1540	CGAAAGGTCAGAAAGACATGGAAGCCAGGTCATCAAAATGGTTTGACTACTTTGTGGACC	1599
Qy	1465	TCTCAAGAGATGCTAGATGAGTCTGATTTGCTTTAAGACCTTACCACACTACGGTCCAGTTA	1524
Db	1600	AATAAGAAGACAGTAGATGAACGAGAAGTCTCTCAAGAACCTGCGACAAAGCTCAGGGGT	1659
Qy	1525	GCCCTCGCCATTGATGTGAACTTTCAGCATCATCAGCAAAAGTCGACTTGTTCAGAGGTGTG	1584
Db	1660	GAGATAGCCATTAAATGTTCACTTGTCCACTCTCGAAGAAAGTGGGCATATTCAGGATTCG	1719
Qy	1585	GATACACAGATGATTTATGACATGTTGCTTAAGATTGAAATCCGTTCTCTATTTCCTGCTG	1644
Db	1720	GAAGCTGGCCTACTGTGGAACTGGTACTGAAGCTTCGTCCTCAGGCTCTTTAGTCCCTGA	1779
Qy	1645	GACTTTGCTGCAAAAAGGGAGAGAAATTTGGCAAGGAAATGTATATCATCAAGATGGAGAA	1704
Db	1780	GATTATATTTCGCTAAGGGGGACATTTGCAAGGAAATGTACATCATCAAGGGGGCAAG	1839
Qy	1705	GTCCAAGTCTCTGGAGGCCCTGATGTGACTAAAGTTCTGGT----TACTCTGAAAGCTGG	1760
Db	1840	TTGGCAGTGGTAGCTGATGATGGCGTGACTCAGTATGCTTCCTGCTCTCAGCTGGGAGCTGC	1899
Qy	1761	GTGGTGTTTGGAGAAATCAGCCCTCTAGCAGCAGGAGGA--GGAAACCGTCAACTGGC	1818
Db	1900	TTTGGTGAGATTTAGTATCCTTAACATTTAAGGTAGCAAAATGGGCNAATCGAGTACTGCT	1959
Qy	1819	AATGTGTGGCCACCGGGTTTGGCAATCTTTTAACTCTTAGACAAAAGACCCCTCCAGAA	1878
Db	1960	AATATCCGTAGCTGGGCTACTCAGATCTCTTCTGCTTGTCTGTCAAAGGACGATCTTATGGAA	2019
Qy	1879	ATTCTAGTGATTTATCCAGATTTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGTCTTTA	1938
Db	2020	GCTGTAACTGAGTATCTGATGCAAGAAAGTCTCTGGAGGAACGGGTAGGAGATCTCTG	2079
Qy	1939	AAGCAGAAGCT	1950
Db	2080	ATGAAGATGGT	2091

RESULT 13
 US-10-295-573-4
 ; Sequence 4, Application US/10295573
 ; Publication No. US20030157571A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Karpen, Jeffrey W.
 ; APPLICANT: Rich, Thomas C.
 ; APPLICANT: Cooper, Dermot M.F.
 ; APPLICANT: Schaack, Jerome
 ; TITLE OF INVENTION: MODIFIED CYCLIC NUCLEOTIDE GATED ION CHANNELS

```

; FILE REFERENCE: UTC-075336
; CURRENT APPLICATION NUMBER: US/10/295,573
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/332,494
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 3027
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-295-573-4

Query Match          5.4%; Score 131.6; DB 15; Length 3027;
Best Local Similarity 46.7%; Pred. No. 7.6e-19; Indels 36; Gaps 5;
Matches 622; Conservative 0; Mismatches 674;

QY 652 TATCTCTGTGGGCTTGTGCTGTGTCACCTCTTGCCTATAACTGGAACCTGCTGGTTATPACCA 711
DB 763 TATTACCGTTGGTGTGTTGTCATTCGCATGCCCTGTCTTTTACAACTGGTGCCCTGTGGTG 822
QY 712 CTGGGCTCTGTCTTCCCATATCAACCGGAGACAAATACATCACTACTGCTTGGCTTATGGGAC 771
DB 823 GCCAGAGCCCTGCTTCAGTGTATCTACAGAGAAACTATTTTGTGTATGGCTGTGGTCTGGAC 882
QY 772 ATCATATGTGATATCACTCACTACCTTTATGATATGCTATTTATCCAGCCCACTCCAGTTT 831
DB 883 TACTTCTCAGACACTGTCTATATCGAGACCTCATCATTCGGCTGGCAGAGC---TTC 939
QY 832 GTAAGAGGAGGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACATACAGGACTTCT 891
DB 940 CTAGAACAGGGGCTCTTGGTCAAAGATCCCAAGAAATTCGGAGACAACTATATTCACACT 999
QY 892 ACAAAATTCAGTTGGATGTCGATCAATAATACCATTTGATATTTGCTACCTCTCTCTT 951
DB 1000 TTGCAGTTCAAATGGAGTGGCTTCTCATCTCCCACTGACCTTATCTATTTTGTCTGTG 1059
QY 952 GGGTT---TAATCCAAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCATTTTTTGA 1008
DB 1060 GGTATCCACAGCCCTGAGGTACGCTTCAACCGTCTATTACACTTTGSCCGTATGTTGAG 1119
QY 1009 TTTAATCATACCTAGAGTCTATAATGGCAAAAGCATATATCTACAGAGTTATTCGAACA 1068
DB 1120 TTTCTTTGACCGCACTGAGACACGACAGCTACGCCCAACATCTTCGAAATCAGCAATCTG 1179
QY 1069 ACTGATACCTGCTGTTTATTTCTGCACATAATGCGCTGTGTTTATTACTGGGCTTCAAAC 1128
DB 1180 GTCCTTTACATCTTGGTCAATCAATCCACTGGAAUGCTGTATTTATATGTTATTTCTAAG 1239
QY 1129 TATGAAGGAATTGG-----CACTACTAGATGGGTGATGAT 1164
DB 1240 TCCATTGCTTTGGAGTTGACACCTGGTTTTACCCCAACATTACTGACCCCTGAATATGGC 1299
QY 1165 GGGGAGGAACAGGATATCTCAGATGTTATTTATTTGGCAGTTTGAACCTTTTAATTACCAT 1224
DB 1300 TACCTGGCTAGAGAGTACATTTACTGTCTTTTACGTGGTCCCACTGACCCCTCACCCACAT 1359
QY 1225 GGTGGCCTTCCAGAACCAACAACCTTTATTTGAAATTTGTTTTCACCTCTTGAATTTTTT 1284
DB 1360 GGAGAGACACACACCCCTGTAAAGGATGAGGAGTACCTATTTGTCACTTTGACTTCTTG 1419
QY 1285 TCTGAGTTTTTGTGTTCTCAGTTTTAATTGGTCAGATGAGAGATGTGATTGGAGCAGCT 1344
DB 1420 ATTGTGTCTCTCATCTTTTGGCAGTATTGTGGGAAATGTGGGCTCCATGATCTCCAAATG 1479
QY 1345 ACAGCCATCAGAACTACTTCCGGCCCTGCAATGATGACACCAATGCTCTACATGAACAAT 1404
DB 1480 AATGCCACACGAGCAGAGTTTCAAGGCCAAGATTGATGCTGTCAACACTACATGCAATTC 1539
QY 1405 TACTCCATTCCCTAACTTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATATACATGGGAC 1464
DB 1540 CGAAAGGTCAGAAAGACATGGAAGCCCAAGGTCATCAATGTTTGTGACTCTTGTGGACC 1599

```

```

RESULT 14
US-09-864-761-12975
Sequence 12975, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED
FILE OF INVENTION: GENE EXPRESSION ANAL
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761,366
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30

```

1465	TCTCAAAGATGCTAGATGAGTCTGATTTCCTTTAAGACCCCTACCAACTACCGGTCCAGTTA	152
QY		
Db		
1600	AATTAAGAGACATAGATGAACGAGAGTCCCTCAGAACCCTGCCAGAAAGCTCAGGCCT	1659
QY		
1525	GCCCTCGCCATTGATGTGAACCTTCAGCATCATCAGCAAGTCGACTTGTTCAAGGGTTGT	1584
QY		
1660	GAGATAGCCATTATATGTTCACTCTTGTCACCTCTGAAGAAAGTCGCCATATTCAGGATTGT	1719
Db		
1585	GATCACACAGATGATTTATGATGATGTTGCTTAAGATTGAAAATCGGTTCTCTATTTCGCTGGT	1644
QY		
1720	GAAGCTGGCCTACTGGTGGAACTGGTACTGAAGCTTCGTCCTCAGGTCCTTAGTCTCTGGA	1779
Db		
1645	GACTTTTGCTGCAAAAAAGGAGGAAAAATGGCAAGAAATGTATATCATCAAGCATGGAGAA	1704
QY		
1780	GATTATATTTGCCGTGAAGGGGACATTTGGCAAGAAATGTACATCATCAAGAGAGGGCAAG	1839
Db		
1705	GTCCAGHTCTTTGAGAGCCCTGATGGTACTAAAGTTCGTGTT---TACTCTCTGAAGAGCTGG	1760
QY		
1840	TTGGCAGTGGTAGCTGANGATGGCGTACTCAGTATTCGCTTCCTCAGCTGGGAGCTGC	1899
Db		
1761	GTGCGTGTTTTGGAGAAATCAGCCCTTTAGCAGCAGGAGGAA--GGAAACCGTCCGAAGCTCC	1818
QY		
1900	TTTGSTGAGATTAGTATTCCTTACAATTAAGGGTAGCAAAATGGCAATCGACGTACTGCT	1955
Db		
1819	AATGTGTGGCCCAAGGGTTTGGCAATCTTTAACTCTAGACAAAAGAACCCCTCCAAGAA	1878
QY		
1960	AATAATCCGTAGCCTGGGCTACTCAGATCTCTTCGTCTGTCCAAGACGATCTTATNGAA	2019
Db		
1879	ATTCTAGTCGATTATTCAGATTTCTGAAGAGGATCCTCATGAAGAAAGCCAGAGTGCTTTTA	1938
QY		
2020	GCTGTAACTGAGTATTCCTGATGCCAAGAGGTCCTGGAGGAACGGGTAGGAGATCCTG	2078
Db		
1939	AAGCAGAGGCCT	1950
QY		
2080	ATGAAGGAAGCT	2091
Db		

RESULT 14
US-09-864-761-12975
; Sequence 12975, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Pern, David R.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

```

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 12975
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013751.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.65
; US-09-864-761-12975

Query Match      5.3%; Score 129; DB 9; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 AGCAAACTCTCCAGAAAAATTCCTGAGAGTCTGACCAACAACTCCGACCTCAAAA 269
DB 191 AGCAAACTCTCCAGAAAAATTCCTGAGAGTCTGACCAACAACTCCGACCTCAAAA 250

QY 270 TGCAGCAGAACCACTGGAACAGTCCAGAGCAGAGCAAGAAATGACCCCGGAAAGG 329
DB 251 TGCAGCAGAACCACTGGAACAGTCCAGAGCAGAGCAAGAAATGACCCCGGAAAGG 310

QY 330 TCCAAACAG 338
DB 311 TCCAAACAG 319

RESULT 15
US-10-087-217-3
; Sequence 3, Application US/10087217
; Publication No. US20030100059A1
; GENERAL INFORMATION:
; APPLICANT: Aptus Genomics, Inc.
; APPLICANT: YAO, Yong
; APPLICANT: CAO, Liang
; TITLE OF INVENTION: No. US20030100059A1el Cell-Based Assays for G-Protein-Coupled Re
; TITLE OF INVENTION: Activities
; FILE REFERENCE: 53735-5004-US
; CURRENT APPLICATION NUMBER: US/10/087,217
; CURRENT FILING DATE: 2002-03-04
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1992)
; OTHER INFORMATION:
; US-10-087-217-3

Query Match      5.3%; Score 128.4; DB 15; Length 1995;
Best Local Similarity 46.5%; Pred. No. 3.2e-18;
Matches 620; Conservative 0; Mismatches 676; Indels 36; Gaps 5;

QY 652 TATCTCTGTGGCTCTTGCTTGTCACTCTTGCTTAATACTGAACTGCTGTTTATACCA 711
DB 424 TATTACCGTTGGTGTGTTGTCATTGCCATGCCCTGTTCTTTACAACTGGTGGCTGTG 483

QY 712 CTGGCGCTCGTCTTCCCATATCAAAACCGAGACAATACACTACTGCTTATTCGGGAC 771
DB 484 GCCAGAGCTGCTTCAGTGATCTACAGAGAACTATTTTGTGATGCTGGTGTGAC 543

QY 772 ATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTT 831
DB 544 TACTTCTCAGACACTGTCTATATCGCAGACCTCATCTTCGGCTGGCAGAGGC---TTC 600

QY 832 GTAAGAGGAGGAGACATAATAGTGGATTCAATAGCTTAAGGAAACACTACAGGACTTCT 891
DB 601 CTAGAACAGGGCTCTTGCTCAAGATCCCAAGAAATTCGAGACAACACTATATTACACT 660

QY 892 ACAAAATTTCACTGATGCTGCATCAATATACCATTTGATATTTGCTACCTCTTCTTT 951
DB 661 TTGCACTTCAAAATGATGCTGCTTCTATCATCTCCACTGACCTTATTTTGTCTGTG 720

QY 952 GGGTT---TAATCCAAATGTTAGAGCAAAATAGGATGTTAAAGTACACATCTTATTTTGA 1008
DB 721 GGTATCCACAGCCCTGAGTAGCTTCAACGCTCTATTACACTTTGCCCGCTATGTTGAG 780

QY 1009 TTATAATCATCACTAGTCTATATATGCAAGAAAGTATATCTACAGAGTTATTTCGAACA 1068
DB 781 TTCTTTGACCGCACTGAGACAGCACCAGCTACCCCAACATCTTCCGAATCAGCAATCTG 840

QY 1069 ACTGGATCTTCTCTTTTATTCTGCACATTAATGCTGCTGTTTATTACTGGCTTCAAA 1128
DB 841 GTCTTTTACATCTTGTCTCATCATCCACTGGAATGCTGTTATTATTATGTTATTCTTA 900

QY 1129 TATGAAGAAATGG-----CACTACTAGATGGGTGTATGAT 1164
DB 901 TCCATTGGCTTTGGAGTTGACACCTGGGTTTACCCCAACATTTACTGACCCCTGAATATGGC 960

QY 1165 GGGGAAGAAACAGATATCTGAGATGTTATTATTATGGGAGTTCGAATTTTAAATACCA 1224
DB 961 TACCTGGCTAGAGATACATTTACTGCTTTTCTGGTCCACACTGACCTCACCACTT 1020

QY 1225 GGTGGCTTCCAGAACCAAACTTTATTGAAATGTTTTCAACTCTTGAATTTTTT 1284
DB 1021 GGAGAGACACCAACCCCTGTAAAGATGAGGAGTACCTATTGTCATCTTTGACTTTCTTG 1080

QY 1285 TCTGGAGTTTTTGTCTTCCAGTTTAAATGGTTCAGATGAGAGATGTCATTTGGAGCAGCT 1344
DB 1081 ATTTGCTTCCTCATCTTTGCCACTATTGTTGGAAATGTTGGGCTCCATGATCTCCAAATG 1140

QY 1345 ACAGCCAAATCAGAACTACTTCCGGCTGTCATGATGATGACACCATTTGCTTACATGAACA 1404
DB 1141 AATGCCACACAGCAGAGTTCCAGGCCAAGATTGATGCTGTCAAACACTACATCAGTTTC 1200

QY 1405 TACTCCATTCCTAACTTGTGCAAAAGGGAGTTCCGGACTTGGTATGATATACATGGGAC 1464
DB 1201 CGAAAGGTCAGCAAGACATGGAAGCCAAAGTCTATCAAAATGTTTGTACTTCTTGTGACC 1260

QY 1465 TCTCAAGAATGCTAGATGAGTCTGATTGCTTGAAGACCCCTTACCAACTAGGGTCCAGTTA 1524
DB 1261 AATAAGAGACAGTAGATGAACGAGAGAGTCTCTCAAGAACCTGCCAGCAAAAGCTCAGGCT 1320

QY 1525 GCCCTCGCCATTGATGAACTTCAGCATATATAGCAAAAGTCTGCTTCAAGGGTTGT 1584
DB 1321 GAGATAGCCATTAAATGTTCACTTGTCCACTCTGAAGAAAGTGGCAGATATTTCCAGGATTGT 1380

QY 1585 GATACACAGATGATTATGACATGTTGTAAGATGAAATCCGTTCTCTATTATTTCCCTGGT 1644
DB 1381 GAAGTGGCTTACTGGTGGAGTCTGACTAGAGCTTCTGCTCCTCAGGCTCTTTAGTCTCTGGA 1440

QY 1645 GACTTTGTCTGCAAAAAGGGAGAAATTTGGCAAGAAATGTATATCATCAAGCATGGAGAA 1704
```

```
Db 1441 GATTATATTGCCGTAAAGGGGACATGGCAAGGAATGTACATCATCAGGAGGCAAG 1500
Qy 1705 GTCCAAAGTTCTTGGAGGCCCTGATGTAATAAGTTCTGGT----TACTCTGAAAGCTCG 1760
Db 1501 TTGGCAGTGGTAGCTGATGATGGCGTGACTCAGTATGCTTGTCTCAGCTGGGAGCTGC 1560
Qy 1761 GTCGGTGTTTGGAGAAATCAGCCTTTAGCAGCAGGAGGA--GGAAACCGTCGAACTGCC 1818
Db 1561 TTTGGTGAGATTAGTATCCTTAACATTAAGGTAGCAAAATGGGCAATCGACGTACTGCT 1620
Qy 1819 AATGTGGTGGCCCAAGGGTTTGCCAAATCTTTTAACTCTAGACAAAAAGACCCCTCCAAGAA 1878
Db 1621 AATATCCGTAGCCTGGGCTACTCAGATCTCTTCTGCTTGTCCAAAGGACGATCTTATGGAA 1680
Qy 1879 ATTCTAGTGCATTATCCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGTCTTTTA 1938
Db 1681 GCTGTAAGTCTGAGGCTCTGTATGCCAAGAGGTCTTGGAGAACGGGTAGGAGATCCTG 1740
Qy 1939 AAGCAGAAGGCT 1950
Db 1741 ATGAAGGAAGGT 1752
```

Search completed: June 22, 2004, 09:37:22
Job time : 1005.63 secs

This Page Blank (uspto)